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Nucleic Acids Res. 14, 8121-8133, 1986 A;Title: Comparison of the late H1 histone genes of the sea urchins: A;Reference number: A25550; MUID:87040778; PMID:3022245 A;Accession: A25550 A;Molecule type: DNA A;Residues: 1-210 <KNO> A;Residues: 1-210 <KNO> A;Cross-references: GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617 C;Superfamily: histone H1 C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus A2550 histone H1 - sea urchin (Lytechinus pictus) C;Species: Lytechinus pictus (painted urchin) C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999 C;Accession: A25550 C;Accession: A25550 R;Knowles, J.A.; Childs, G.J. Ś 맑 RESULT 1 Matches Query Match Best Local Similarity 166 АККААККРААККРАККААККРААККААКРАККААККРААККАА 208 28; 1 АККҮАККАКАЕК-АККАҮКААЕАККААКҮЕКАААЕКАААКЕАА 42 Conservative 48.6%; Mismatches Score 103.5; DB Pred. No. 0.0053; DB 2; 11; Length 210; Indels sea urchins Lytechinus pictus 1; Gaps 1;

A;Molecule type: DNA A;Residues: 1-394 <HAY> A;Crose-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154 A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics: R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796 membrane spanning protein TolA [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: F90725 á F90725 Query Match Best Local S Matches 32 EC80774 32; Conser Conservative 46.0%; Score 98; DB 2; Pred. No. 0.028; 2; Mismatches 9, Length 394; Indels 45 6 Gaps ü ი ი geno

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KKAAEKAAAEKAAADKKAAAEKAAADKKAAA-AKAAAEKAAAAKAAAEA 267

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C;Keywords: nucleotide binding; P-loop; transmembrane F;14-34/Domain: transmembrane #status predicted <MSS>F;78-301/Domain: helical #status predicted <HSR>F;35-362/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960 A;Experimental source: strain K-12, substrain MG1655 C;Comment: tolA and tolB proteins are necessary for colicins E2, E3, A, and K to reach 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019
A;Experimental source: strain JM105
A;Note: the authors translated the initiation codon GTG for residue 1 as
A;Note: the authors translated the initiation codon GTG for residue 1 as
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002 C;Accession: JV0057; B64810 R;Levengood, S.K.; Webster, R.E. J. Bacteriol. 171, 6600-6609, 1989 J. Bacteriol. 171, 6600-6609, 1989 A;Title: Nucleotide sequences of the tolA and tolB genes and localization o A;Reference number: JV0057; MUID:90078104; PMID:2687247 A;Accession: JV0057
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                membrane spanning protein TolA [imported] - Escherichia coli (strain O157:H C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Nov-2001 C;Accession: G85576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64810
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A;Residues: 1-394 <STO>
A;Cross-references: GB.AE005174; NID:g12513672; PIDN:AAG55075.1;
A;Experimental source: strain O157:H7, substrain EDL933
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A;Accession: G85576
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A; Residues: 1-421 <LEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: nucleic acid sequence not shown; translation not shown
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Science 294, 849-852, 2001
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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein homolog lin2055 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua (C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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A;Experimental source: strain Clip11262
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A; Residues: 1-243 <GLA>
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A;Cross-references: GB:NC_003210; PIDN:CAD00019.1;
A;Experimental source: strain EGD-e
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.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihi,
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       39 KEAAYE 44
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                                                                                                                                                                                                                                                 42.3%;
                                                                                                                                                                                                                    Score 90; DB 2
Pred. No. 0.11;
3; Mismatches
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Pred. No. 0.04;
7; Mismatches
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; Entian, K.D.;
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Voss, H.; Wehland,
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Fsihi, H.
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Fsihi, H.
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Wehland,
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R;Neesen, J.; Padmanabhan, S.; Buenemann, H. Eur. J. Biochem. 225, 1089-1095, 1994
A;Title: Tandemly arranged repeats of a novel highly charged lpha-helical rods within the extremely elongated spermatozoa A;Reference number: S51364; MUID:95045538; PMID:7957199
                                                                                                                                  probable hup8 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: G70673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional A;Reference number: A28100; MUID:88246461; PMID:2837660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X73481
R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H.
submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Drosophila hydei
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S51364; S34154
                           R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                 G70673
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A; Residues: 1-211 <LAI>
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A;Residues: 1-163,'E',164-236,'Q',237-254,257-320,'E',321-1390 <NEW>
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
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                                                                                                                                                                                                                                                                       RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB:M20314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A28100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          histone H1-beta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: FlyBase:FBgn0011816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1390 <NEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           istone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus)
;Species: Strongylocentrotus purpuratus (purple urchin)
;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Accession: A28100
;Lai, Z.C.; Childs, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Status: nucleic acid sequence
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 42.3%;
Similarity 57.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KETAEKKKCEKAAKKRKEAAEKKKCAEAAKKEKEAAEKKKCEEAA
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  Sulston, J.E.; Taylor, K.; Whitehead,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.0%; Score 89.5; DB 2; Length 211; 61.9%; Pred. No. 0.11; tive 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       not shown
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Pred. No. 0.41;
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S.; Barrell, B.G
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of Drosophila hydei.
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A; Molecule type: DNA A; Residues: 1-384 <YEL> A; Residues: 1-384 <YEL> A; Residues: 1-384 <YEL> A; Cross-references: GB: M58563; NID: g155066; PIDN: AAA27480.1; PID: g155067 A; Note: the authors translated the codon TTC for residue 316 as Tyr, and C; Keywords: membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4116-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-214 < COL>
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                                                                                                                                                                                                                           R;Yelton, D.B.; Limberger, R.J.; Curci, K.; Malinosky-Rummell, F.; Slivienski, L.; Scho Infect. Immun. 59, 3685-3693, 1991
A;Title: Treponema phagedenis encodes and expresses homologs of the Treponema pallidum A;Reference number: A43592; MUID:91372983; PMID:1894368
                                                                                                                                                                                                                                                                                                                      C;Species: Treponema phagedenis
C;Date: 30-Jan-1993 #sequence_revision
C;Accession: B43592
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B43592
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C;Superfamily: bacterial type I DNA topoisomerase
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C;Superfamily: histone H1
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A;Residues: 1-899 <STO>
A;Cross-references: GB:AE005673; NID:g13423998; PIDN:AAK24422.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87553
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                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                        A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                       outer membrane protein TmpB - Treponema phagedenis
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKKPAKKAAATKSKAKAESDAPAKKTAA-KKPAAKKPAAKKAAPKA 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       АККУАККАКАЕКАК-КАУКААЕАККААКУЕКАААЕКАААКЕААУЕА 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA
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40.6%;
54.5%;
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55.6%;
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Pred. No.
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  Score 86.5; DB 2; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                            12-Mar-1993 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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                       Length 384;
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RESULT 13
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A;Authbors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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C;Accession: E83525
R;Stover, C.K.; Pham, X.Q.; Erwin, adman, S.; Yuan, Y.; Brody, L.L.; (
,; Lory, S.; Olson, M.V.
                                                                                                                                      TolA protein PA0971 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa (c;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #sequ
                                                                                                                                                                                                                                                                 RESULT 14
E83525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references:
C;Superfamily: neuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Neesen, J.; Heinlein, U.A.O.; Buenemann, H. submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mst101-1 protein - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: FlyBase:Dhyd/mst101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S34153
A; Accession: S34153
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ККААРАККААРАККААРАККАРАККАА 192
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neurofilament triplet H
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                                      Coulter,
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                                                                            A.L.;
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                                  hi, S.D.; Warrener, Folger, K.R.; Kas,
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K.; Lim,
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Search completed: Job time : 9.1818;

January 12 secs

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RESULT 15
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A;Molecule type: DNA
A;Residues: 1-347 <STO>
A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; GSPDB:GN001
A:Ernerimental source: strain PAO1
                                                                                                                                                                                                                                                                                                      R;Scarlato, V.; Arico, B.; Goyard, S.; Ricci, S.; Manetti, R.; Prugnola, A.; Manetti, R Mol. Microbiol. 15, 871-881, 1958
A;Title: A novel chromatin-forming histone H1 homologue is encoded by a dispensable and A;Reference number: S61926; MUID:95319329; PMID:7596289
A;Accession: S61926
                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 23-Jul-1996 #sequence_revision 06-Sep-1996 #text_change 24-Nov-1999 C;Accession: S61926; S69327
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A;Accession: E83525
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                                S
                                                                                                                                           C; Superfamily: histone H1
                                                                                                                                                              A;Gene:
                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 'X', 3-39 <SCA2>
                                                                                                                                                                                                                                A;Cross-references: EMBL:L37438;
A;Accession: S69327
                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-182 < SCAl>
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Similarity 61.4%;
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                                                                                      Score 85; DB 2
Pred. No. 0.25;
                                                                       Mismatches
                                                                                                         DB 2;
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                                                                                                         Length 182;
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Query Match Best Local S Matches 28

Similarity

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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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TOLA_
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                                                                                     Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A., "Filamentous phage infection: crystal structure of g3p with its coreceptor, the C-terminal domain of TolA."; Structure 7:711-722(1999)
                                                                                                                                                                              "TolA central domain intera
EMBO J. 15:6408-6415(1996).
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"Nucleotide sequences of the tolA and tolB genes and localization their products, components of a multistep translocation system in Escherichia coli.";
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Lloubes R.;
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Levengood S.K., Beyer W.F. Jr., Webster R.E.;
"TolA: a membrane protein involved in colicin
extended helical region.";
Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(199
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MEDLINE=97133271; PubMed=8978668;
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Science 277:1453-1474(1997).
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                                                                                                                                      MEDLINE=99332679; PubMed=10404600;
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           BINDING TO THE BACTERIA. ALSO INVOLVED OF BACTERIOPHAGE DNA.
SUBUNIT: INTERACTS, VIA DOMAIN II, WITH
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COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL
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                                                  Neesen J., Padmanabhan S., Buenemann H.;
"Tandemly arranged repeats of a novel highly charged 16-amino-acid
motif representing the major component of the sperm-tail-specific
axoneme-associated protein family Dhmst101 form extended
alpha-helical rods within the extremely elongated spermatozoa of
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PIR; JV0057; JV0057.
PDB; 1TOL; 20-MAY-99.
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                                                                                                                                                        SEQUENCE FROM N.A., AND CHARACTERIZATION MEDLINE=95045538; PubMed=7957199;
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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Pred. No. 0.00
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PERIPLASMIC (POTENTIAL).

DOMAIN II (ALPHA-HELICAL).

DOMAIN III (FUNCTIONAL).

10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriocin transport; Transmembrane; ructure; Complete proteome.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8B2F52B4B97C655E CRC64;
  ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                      1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
0.0073;
  Ï
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    THE
                                                                                                                                                                                                                                                                             Insecta; Pterygota;
    SPERM
                                                                                                                                                                                                                                                          Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294
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DESCRIPTION OF THE PROPERTY OF
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       smegmatis.";
Mol. Gen. Ger
-!- FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last annotation update)
DNA-binding protein HU homolog (Histone-like protein) (Hlp)
HUP OR HLP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                              InterFio; ____ DNA
Pfam; PF00216; Bac_DNA
___ DN000945; Bac_
                                                                                                                                              EMBL; AF068138; AAD13809.1; -. HSSP; P02346; 1HUU.
                                                                                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 700084 / mc(2)155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterineae; Mycobacteriaceae; Mycobacterium
NCBI_TaxID=1772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Upregulation of a histone-like protein in dormant Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99110209; PubMed=9894918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DBH_MYCSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gen. Genet. 260:475-479(1998).
FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMILY OF PROKARYOTIC DNA-BIJDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DIFFERENT
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WITHIN TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: SPERMATIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                         European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboratio een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content is in no war by non-profit institutions as long as its content in the long 
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Repeat; Multigene family; Polymorphism.

Repeat; Multigene family; Approximate Tandem REPEATS

32 1268 [KR]-K-X-C-X-X-A-K-X-X-K-X-X-X-E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X73481; CAA51876.1; -.
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IPRO00119; Bac DNAbind.
0216; Bac DNA binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murugasu-Oei B., Dick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1391 AA;
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(Rel.
(Rel.
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Bac_DNAbind;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.3%;
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; Pred. No. 0.13
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                         . Usage by and for http://www.isb-sib.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
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                                                                                                                                                                                                                                                                                                                                    for commercia.
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                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00411; BHL; 1.

PROSITE; P800045; HISTONE LIKE; 1.

DNA-binding; DNA condensation; Repeat.

DOMAIN 1 90 BACTERIAL HISTONE-LIKE DOMAIN.

DOMAIN 1 205 DEGENERATE REPEATS REGION.

CASP577P61F7EF09 CRC64;
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a colla between the Swiss Institute of Bioinformatics and the EMBL outs the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for coentities requires a license agreement (See http://www.isb-sib.ch/a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H1B_STRPU
P15869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Last seque 15-JUL-1999 (Rel. 38, Last annot Histone H1-beta, late embryonic
                                                                                                                                                                                                                                        EMBL; M20314; AAA30052.1; -. PIR; A28100; A28100. HSSP; P02259; 1HST.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Strongylocentrotus purpuratus.";
MO1. Cell. Biol. 8:1842-1844(1988).
-i- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus purpuratus (Purple sea urchin).
Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Buechioidea; Echinacea; Echinoida; Strongylocentrotidae;
Strongylocentrotus.
                                                                                                                                        ProDom; PD000373; L1
SMART; SM00526; H15;
                                                                                                                                                                   InterPro; IPR005819; Histone-H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; linker histone; I.
PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                                                 or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the gene encoding the late histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=88246461; PubMed=2837660;
Lai Z.-C., Childs G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990
01-APR-1990
                                                                                                                                                                                                                            InterPro; IPR005818; Histone_H1/H5.
                                                                                                                                                                                                                                                                                                                                                                                                                - 1 - SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization
                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111
 139
                                                        26; Conser
                                                                                                                                                                                                                                                                                                 g requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                       PD000373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKKAAKKAPAKKAAAKKTATKAAAKKAPAKKAATKAPAKKAATKAPAKKAATKA
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SKKTTKKVKKPAAKKAKKPA-AKKAAK--KPAAKKPAAKKAA 177
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                                                                                                                            protein;
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of the structure
                                                                                                             ; Nuclear protein; 22169 MW; 9F21458
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61.9%;
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53.7%;
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                                                   Score 89.5; D
Pred. No. 0.02
3; Mismatches
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                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                               DNA-binding; Multigene family.
31334BBE7A CRC64;
                                                                     0.026;
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DBH_MYC
P95109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999
15-JUL-1999
16-OCT-2001
ProDom; PUVVVIII
SMART; SM00411; BHL; 1.
PPOSITE; PS00045; HISTONE LIKE; 1.
                                                   InterPro; IPR000119; Bac_DNAbind.
InterPro; IPR005819; Histone H5.
Pfam; PF00216; Bac_DNA_binding; 1.
PRINTS; PR00624; HISTONEH5.
PRODOm; PD000945; Bac_DNAbind; 1.
                                                                                                                                                                                      EMBL; Z83018; CAB05427.1; -. EMBL; AE007127; AAK47393.1;
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Peterson J., DeBoy R., Dodson W. Gwinn
Kolonay J.F., Nelson W.C., Umayam L.A.,
Delcher A., Utterback T., Weidman J., Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding protein HU homolog (Histone-like laminin-2-binding protein).
HUP OR HLP OR LBP21 OR RV2986C OR MT3064 OR I
                                                                                                                                            TIGR; MT3064;
                                                                                                                                                                                                                                   or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prasad H.K., Annapurna P.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=H37Rv;
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                                                                                                                           TubercuList; Rv2986c;
                                                                                                                                                                          PIR; G70673; G70673.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                  mitted (DEC-1997) to the SWISS-PROT data bank. FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE FAMILY OF PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WRAPPING DNA TO STRABILIZE IT, AND PREVENT ITS DENATURATION UNDER EXTREME ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
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                                                                                                                                                                                                                                 non-profit institutions as long and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF 71-86, AND DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (APR-2001)
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         DNA condensation; Repeat; Complete proteome
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Gwinn M.L., Haft D., Hickey E.,
L.A., Ermolaeva M.D., Salzberg
J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
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Matches 25
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STRAIN=91372983; PubMed=1894368;
Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W.
"Treponema phagedenis encodes and expresses homologs of t pallidum TmpA and TmpB proteins.";
Tnfect. Immun. 59:3685-3693(1991).
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             REPEAT
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01-APR-1993 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Bacteria; Spirochaetes;
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                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: TMP MAY SERVE LARGE MOLECULES.
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Protein B precursor (An
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SEQUENCE FROM N.A.
STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Kawarabayasi Y., Yamazaki J., Itoh T., Yamagishi
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ProDom; PD003791; Ribosomal_S16; 1.
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PROSITE; PS00732; RIBOSOMAL_S16; FALSE_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterineae; Corynebacteriaceae; Corynebacterium
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                                                                                                                                                                                                                                                                                                                                                                    mitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
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384 AA;
(Rel. 34, (Rel. 34,
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Pred. No. 0.04
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RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the Tracomplete genome sequence.";
IL Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Pleischmann R.D., Hickey E., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Kolonay J.F., Nelson W.C., Umayam J., Khouri H., Gill J., Mikula pelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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SPECIES=M.tuberculosis, and M.bov
STRAIN=437Rv, ATCC 201 / H37Ra, a
MEDLINE=98445421; PubMed=9770536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last annotation update) Heparin-binding hemagglutinin (Adhesin). HBHA OR RV0475 OR MT0493 OR MTCY20G9.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-16, AND CHARACTERIZATION.
SPECIES=M.tuberculosis, and M.bovis;
STRAIN=ATCC 201 / H37Ra, and BCG / Paris 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=M.tuberculosis;
MEDLINE=98295987; PubMec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES=M.tuberculosis, and M.bovis; STRAIN=103, and BCG;
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                                                                                                                                                                                                                                                                                     extrapulmonary dissemination.";
Nature 412:190-194(2001).
                                                                                                                                                                                                                                                                                                                                                                                                            Pethe K.
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21342355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of a heparin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Menozzi F.D., Rouse o
Bischoff R., Brennan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97188915; PubMed=9064359;
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                                                                                                                                                                                                                                                                                                                                                  "The heparin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tuberculosis clinical and
FUNCTION: REQUIRED FOR EXTRAPULMONARY DISSEMINATION. MEDIATES ADHERNOE TO EPITHELIAL CELLS BY BINDING TO SULFATED GLYCOCONJUGATES PRESENT AT THE SURFACE OF THESE CELLS; BINDS HEPARIN, DEXYRAN SULFATE, FUCCIDAN AND CHONDROITIN SULFATE. PROMOTES HEMAGGLUTINATION OF ERYTHROCYTES OF CERTAIN HOST SPECIES. PROMOTES HEMAGGLUTINATION OF ERYTHROCYTES OF CERTAIN HOST SPECIES. INDUCES MYCOBACTERIAL AGGREGATION.
SUBCELLULAR LOCATION: SURFACE ASSOCIATED.
DOMAIN: HEPARIN BINDING SEEMS TO REQUIRE THE C-TERMINAL DOMAIN OF HEHA. PROGRESSIVE TRUNCATIONS FROM THE C-TERMINAL END
                                                                                                                                                                                                                                                                                                                                                                                                               Alonso
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3rennan M.J., Locht C.;
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R., Parkhill J., Ga
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                                                                                                                    "The Drosophila hydei gene Dhmst101(1) encodes a testis-specific, repetitive, axoneme-associated protein with differential abundance Y chromosomal deletion mutant flies.";
Dev. Biol. 162:414-425(1994).
-i- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL. IT IS
                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995
16-OCT-2001
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                                                                                                                                                                                          Neesen J., Buenemann H.,
                                                                                                                                                                                                                                                                           Ephydroidea;
                                                                                                                                                                                                                                                                                        Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                 Drosophila hydei (Fruit fly)
                                                                                                                                                                                                                                                                                                                              MST101(1).
                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
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                                                                                                                                                                                                      MEDLINE=94200512; PubMed=8150205;
                                         POLYMORPHISM:
                                                                                         ASSOCIATED WITH AXONEMAL STRUCTURES SUBCELLULAR LOCATION: Cytoplasmic ()
                                                                 TISSUE SPECIFICITY: TESTIS. SPERMATID BUNDLES.
                                                      DOMAIN: THE PREDOMINANT STRUCTURE IS
                                                                                                                                                                                                                                                                                                                                                                                                             DROHY
SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                        Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                       31, Created)31, Last sequence update)40, Last annotation update)
                                       THE NUMBER OF REPEATS VARIES
                                                                                                                                                                                                                                                                                                                                            protein mst101(1).
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                                                       ALPHA-HELICAL
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                                                                                                                                                                                                                                                                                        Muscomorpha;
                                      BETWEEN STRAINS.
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            collaboration
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RESULT 11
TOLA_PSEAE
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This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                        MEDLINE=20437337, PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Weetbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X73480; CAA51875.1; -. PIR; S34153; S34153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                 opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                      Dennis J.J., Lafontaine E.R., Sokol I "Identification and characterization Pseudomonas aeruginosa.", J. Bacteriol. 178:7059-7068 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P50600;
01-OCT-1996
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Sperm; Repeat; Multigene family.
DOMAIN 58 337 19 X 16
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                                                                                                                                                                                                                                                                                                         STRAIN-ATCC
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Duan K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
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TOLA OR PA0971
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                                                                                                                                                                                            "Complete genome sequence of Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                            REVISIONS TO N-TERMINUS.
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SUBCELLULAR LOCATION:
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Pred. No. 0.
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Query Match Best Local S Matches 21

Similarity

40.4%;

Score 86; Pred. No.

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Length 198

Conservative

4.

Mismatches

7;

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DOMAIN CONFLICT

193 # 120 # 21403 MW;

ALA/LYS-RICH. R -> P (IN REF. 1). ; 513760F6F1EB6042 CRC64;

Cell

adhesion; Heparin-binding; Hemagglutinin;

Glycoprotein,

irulence;

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Complete proteome

TubercuList;

Rv0475; -.

TIGR; MT0493;

EMBL; AF074390; AAC26052.1; -.
EMBL; Z77162; CAB00936.1; -.
EMBL; AE006951; AAK44716.1; AL7
PIR; F70742; F70742.

AAK44716.1; ALT_INIT

SEQUENCE

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the European Bioinformatics Institute.

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(See http://www.isb-sib.ch/announce/

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European Bioinformatics Institute.

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collaboration -

SIMILARITY: STRONG, TO M. LEPRAE HBHA.

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Matches 24
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Q9X5I8; Q9S5U5;

16-OCT-2001 (Rel. 40, Last seq

16-OCT-2001 (Rel. 40, Last seq

16-OCT-2001 (Rel. 40, Last ann
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SEQUENCE
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EMBL; AE004530; AAG04360.1;
PIR; E83525; E83525.
                        InterPro; IPRO00119; Bac_DNAbind.
InterPro; IPRO05819; Histone H5.
Pfam; PF00216; Bac_DNA binding; 1.
PRINTS; PR00624; HISTONEH5.
ProDom; PD000945; Bac_DNAbind; 1.
SMART; SM00411; BHL; 1.
                                                                                                                                                                             EMBL; Y18421; CAB46493.1; -.
EMBL; AB013441; BAA78330.1;
HSSP; P02346; 1HUU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prabhakar S., Tyagi J.S., Prasad H.K.; "HLPMt-A target for differentiation of M.tuberculosis and M.bovis."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1765;
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TIGRFAMs; TIGR01352; tonB_Cterm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification of a novel protein generating bacterial slow from Mycobacterium.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-I-FUNCTION: THIS PROTEIN BELONGS TO THE HISTONE LIKE FAMIL PROKARYOTIC DNA-BINDING PROTEINS WHICH ARE CAPABLE OF WR DNA TO STABILIZE IT, AND PREVENT ITS DENATURATION UNDER ENVIRONMENTAL CONDITIONS (BY SIMILARITY).
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HISTONE_LIKE; 1
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OF WRAPPING
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RESULT 14 H1_PARAN

SEPPPR SEPPR

Histone H1, gonadal.

Parechinus angulosus (Angulate sea urchin).

Eukaryota; Metazoa; Echinodermata; Eleutherozoa;

Echinozoa;

H1 PARAN P02256; 21-JUL-1986 21-JUL-1986 15-JUL-1999

STANDARD;

PRT;

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                                                                                                 Query Match
Best Local Similarity .
Matches 22; Conserva
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Best Local
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Q8NNX3;
28-FEB-2003
28-FEB-2003
28-FEB-2003
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                        TIGRPAMS; TIGR00002; S16; 1.

PROSITE; PS00732; RIBOSOMAL S16; FALSE NEG.
RIBOSOMAL PROTECTION; COMPLETE PROTECOME.

SEQUENCE 165 AA; 17837 MW; 61DD81961BC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA-binding; DNA condensation; Repeat.

DOMAIN 1 90 BACTERIAL HISTONE-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genomic sequence of Corynebacterium glutamicum ATCC 130 Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                               HAMAP; MF_00385; -; 1
InterPro; IPR00307; Ribosomal_S16.
Pfam; PF00886; Ribosomal_S16; 1.
ProDom; PD003791; Ribosomal_S16; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP005280; BAB99447.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corynebacterium glutamicum (Brevibacterium flavum)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1718;
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120
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3 (Rel. 41, Last a
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199
205 AA;
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annotation update)
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Pred. No. 0.061;
2; Mismatches
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                                                                                                    Score 82; DB 1
Pred. No. 0.11;
4; Mismatches
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152
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RESULT 15
H1E_CHIPA
ID H1E_CHIPA
AC P40262;
DT 01-FEB-1995
  CCCCCFFFRXCOCCCCFFF
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Best Local
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                                                                                           SEQUENCE FROM N.A.

Schulze E., Wisniewski J.R., Nagel S., Gavenis K., Grossbach
Submitted (XXX-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A91090; HSURIP.
HSSP; P02259; 1HST.
InterPro; IPR005818; Histone_H1/H5.
InterPro; IPR005819; Histone_H5.
InterPro; IPR003216; Linkerhist_N.
Pfam; PF00538; linker histone; 1.
  This
                                                                                                                                                                                                                                                                         Chironomus pallidivittatus (Midge).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Chironomoidea;
Chironomidae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                    Histone H1E.
                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 2. Sequence of the C-terminal CNBr peptide at the entire primary structure."
Eur. J. Biochem. 104:567-578(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=80156832; PubMed=7363905; Strickland W.N., Strickland M., B Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cyanogen bromide peptides.";
Eur. J. Biochem. 104:559-566(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of the protein and the sequence of amino acids in the four N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=80156831; PubMed=6767609; Strickland W.N., Strickland M., de Groot P.C., Wittmann-Liebold B.;
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NCBI_TaxID=7658;
                                                                                                                                                                                                                                                      NCBI_TaxID=7151;
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                                               SUBCELLULAR LOCATION: Nuclear SIMILARITY: BELONGS TO THE HIS
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SWISS-PROT entry is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144
248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; Nuclear protein; DNA-binding; Multigene
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                                                 TO THE HISTONE H1/H5 FAMILY.
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Pred. No.
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produced through
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  collaboration
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ProDom; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
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152; 258796; Shi M., Kuryama K., Mu. Yama K., Mu. Yama K., Shina ii M., Shina if enterohemu. son with a	TCC 700927; 206551; Burland V Ins P.S., Grik S., Bouting P.S., Grik S., Bouting Lim A., Dim S., Lin J., S., Lin J.,	PRT; 394 AA. (), Created) (), Last sequence update (), Last annotation upda (), required for outer me () TOLA). Gammaproteobacteria; E
[2] SEQUENCE FROM N.A. STRAIN=O157:H7 / RIMD 0509952; STRAIN=O157:H7 / RIMD 0509952; MEDLINE=21156231; PubMed=11258796; MEDLINE=21156231; PubMed=11258796; MEDLINE=21156231; PubMed=11258796; MEDLINE=21156231; PubMed=11258796; MEDLINE=21156231; PubMed=11258796; MITCHARD E., MAKAYAMB K., MURATA T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sabakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Kuhara S., Shiba T., Hattori M., Shinagawa H.; TCHARDIA ESCHERICA COLI "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001). DNA Res. 8:11-22(2001). EMBL; AB005252; AAG55075.1;	[1] SEQUENCE FROM N.A. STRAIN=0157:H7 / EDL933 / ATCC 700927; STRAIN=0157:H7 / EDL933 / ATCC 700927; MEDLINE=21074935; PubMed=11206551; Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533 (2001).	PRT; 394 AA. Created) Last sequence update) Last annotation update) required for outer membrane integrity TolA). TolA: ammaproteobacteria; Enterobacteriales; chia.

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Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., S Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome of uropathogenic Bacherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
Domann E., Domann E., Esihi H., Entian K.-D., Fsihi H., Goebel W.,
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PRINTS; PR00308; ANTIFREEZEI.
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SEQUENCE 394 AA; 40517 MW:
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
             Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T., Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussur Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jack
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MEDLINE=21537279; PubMed=11679669;
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Q92A67; Q92A67; 01-DEC-2001 01-DEC-2001 01-MAR-2003

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

19, 19, 23,

Created)

Last sequence update)
Last annotation update)

PRELIMINARY;

243

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RESULT 5
Q92A67
ID Q92A
AC Q92A
DT 01-D
DT 01-D
DT 01-M
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Q9AJX2
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
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InterPro; IPR002402; LysM.
Pfam; pF01476; LysM; 1.
SMART; SM00257; LysM; 1.
Hypothetical protein; Complete p:
SEQUENCE 239 AA; 25836 MW; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9AJX2
Q9AJX2;
Q1-JUN-2001 (TEMBLrel. 17,
01-JUN-2001 (TEMBLrel. 17,
01-MAR-2003 (TEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kura Madueno B., Maitournam A., Mata Vicente J., Ng E., Nedjar Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P., "Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=A3(2) / M14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomycineae; Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCO1805 OR SCI33.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL591981; CAD00019.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 417:141-147(2002).
EMBL; AL939110; CAC28545.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteome.
                                                                                                                                                                                                                                     SOKVAAIEAKKEAAAKKATAKKATAEKKAAAEKAAAKRAAKE 119
                                                                                                                                                                                                                                                                                            AKKAKAEKAKK--AYKAAEAKKAAKYEKAAAEKAAAKEAAYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KAAAEKAEADKKKQEEDAVKAANAKKEQEAAEEKAAADKAAAEKAAAE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.4%;
nilarity 56.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 AA;
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25524 MW;
                                                                                                                                                                                                                                                                                                                                                                         42.7%;
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                                                                                                                                                                                                                                                                                                                                              Score 91; DB Pred. No. 0.1; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 94.5; DB 1
Pred. No. 0.045;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteome.
72E59D576E0D7832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61999D62CA23A7B0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces
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                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kurapkat G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44
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Best Local S
Matches 30
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01-JUL-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Axoneme-associated protein MST101(3)
MST101(3) OR DHMST101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baguero F., Berche P., Bloecker H., Brandt P., Chakraborty T., Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P., Convent Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Esntian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H., Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., Varguez-Boland J.-A., Voss H., Wehland J., Cossart P.;
                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                             Neesen J., Heinlein U.A.O., Buenemann H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL
  SEQUENCE
                                                                                EMBL; U85627; AAB51369.1;
                                                                                               SIMILARITY).
-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: TESTIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                 Drosophila hydei (Fruit fly).
                                                                                                                                                                                                                                                                                                                                             001395;
                                                                                                                                                                                                                                                                                                                                                            001395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 294:849-852(2001).
EMBL; AL596170; CAC97285.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glaser P., Frangeul L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CLIP 11262
PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
LIN2055.
                                                                   FlyBase;
                                                                                          -!- TISSUE SPECIFICITY: TESTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Listeria innocua.
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Comparative genomics of Listeria species.";
                                                                                                                                                                                                          CBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                            166 DKAAKE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106
                                         Repeat; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                      39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKKAAEEKAAAEKKAAEEKKAAEKKAADKKSQEDEAAKAAAAKKEQEAAEEKAAAEKAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKKYA-KKAKAEKAKKAYKAAEAKKA-----
                                                                 FBgn0020732; Dhyd\mst101(3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Firmicutes;
  275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein lin2055
                                       ; Multigene
64 255
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    30436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchrieser C., Rusniok C.,
                                                      family
    ₹,
                                                                                           STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.13
3; Mismatches
                          13 X 16 AA APPROXIMATE TANDEM REPEATS X-[KQ]]-K-C-[AE]-E-X-A-[X]-K-X-X-X-X-
[AE]-X.
76BAA7B2A2DF732C CRC64;
                                                                                                                                                                                                                                                                                                                                                            275 AA
                                                                                          SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 243;
                                                                                           ALPHA-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----АКҮЕКАЛАЕКАЛА 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                              YB)
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RESULT 8
Q9A5J6
ID Q9A5
AC Q9A5

Q9A5J6;

PRELIMINARY;

PRT;

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RESULT 7
Q9WWYXI
DD Q9WW
AC Q9WWYXI
DT 01-W
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                              Matches
                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The Pseudomonas putida peptidoglycan-associated out
lipoprotein (PAL) is involved in maintenance of the
cell envelope.";
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01-MAR-2003
                                                                                                                                                                                                                                                                   TIGRFAMB; TIGR01352; tonB_Cterm; SEQUENCE 372 AA; 40133 MW; 8
                                                                                                                                                                                                                                                                                                         InterPro; IPR005819; Histone_H5.
InterPro; IPR006260; TonB_C.
PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                                                                                                                                   Rodriguez-Herva J.J., Ramos J.;
"Characterization of an OprL null mutant
J. Bacteriol. 178:5836-5840(1996).
EMBL; X74218; CAB50780.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rodriguez-Herva J.J.;
Submitted (JUL-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ramos-Gonzalez I.;
Submitted (JUN-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tolk protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9WWX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96422022; PubMed=8824639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=mt-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96198174; PubMed=8626299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas putida.
Bacteria; Proteobacteria;
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181
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                                                                                     AEDAAKAAEAAKAAEAKKAAEAKKADEAKKAAEKQQADIAKKKAEDEAKKKAEEEAKKAA 180
AEEAKKKA 188
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Pred. No. 0.27
8; Mismatches
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Last seq
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Last annotation updat
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Matches 27
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Pfam; PF01751; Toprim; 1.
Pfam; PF01396; Zf-C4 Topoisom; 1.
PRINTS; PR00417; PRTPISMRASEI.
SMART; SM00437; TOP1BC; 1.
SMART; SM00433; TOP1BC; 1.
SMART; SM00433; TOPRIM; 1.
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Q1-MAR-2002 (TrEMBLrel. 2

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Probable histone H1 prote

RSC2793 OR RSO0453.
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01-JUN-2001 (TrEMBL
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DNA topoisomerase (
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Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

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DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

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"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

-1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE

CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=ATCC 19089 /
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                                                                                                                                                                                                                                                                                                                                                 DNA-binding; Isomerase; Topoisomerase; SEQUENCE 899 AA; 97723 MW; 1485DC4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003601; DNAtopI ATP_bind.
InterPro; IPR003602; DNAtopI DNA_bind.
InterPro; IPR003733; DNA_topI bact.
InterPro; IPR00330; DNA_topisomrase.
InterPro; IPR006171; Toprim_dom.
InterPro; IPR006154; Toprim_sub.
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PROSITE; PS00396; TOPOISOMERASE_I_PROX; 1.
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SIMILARITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED CAPALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED DNA, FOLLOWED BY PASSAGE AND REJOINING.

MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA ALKEONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN JUNA LINK, IN MACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN JUNA LINK, IN WHICH A TYROSYL OXYGEN IN THE BUZYME 15 JOINED TO A DNA PHOSPHORUS AT ONE END OF THE ENZYME-SEVERED DNA STRAND (BY SIMILARITY).

SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAMILY
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P06612; IECL.
CC2451; -.
                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                           AKKYAKKAKAEKAK-KAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
solanacearum (Pseudomonas solanacearum)
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
merase (EC 5.99.1.2).
                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                              Conservative
                                H1 protein
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5; Mismatches
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1485DC4EDA0DA6FA CRC64;
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0.71;
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                                                                                                                                                                                                                                                                                                             Length 899;
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RESULT 10
Q8PI40
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                                                                                                                                                                                                                                                                                                                                                     RA da Silva A.C.R., Perro J.A., Reinach F.C., Farah C.S., Furlan L.R., RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camaryo L.E.A., Alves L.M.C., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P., RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Furber A., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Ratsuyama A.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Martins E.C., Medanis J., Menck C.F.M., Miyaki C.Y., Moon D.H., A.M., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Pereira H.A., Rossi A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Tindade dos Santos M., Truffi D., Tsai S.M., White F.F., Tomparison of the genomes of two Xanthomonas pathogens with differing Not specificities.";
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Q8P140;
01-OCT-2002
01-OCT-2002
01-MAR-2003
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EMBL; AL646071; CAD16500.1; -.

InterPro; IPR005819; Histone_H5.

PRINTS; PR00624; HISTONEH5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=306 / ATCC
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                                                                                                                                                                                                                                                                                   Nature 417:459-463(2002).
EMBL; AE011948; AAM37903.1;
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MEDLINE=22022145; PubMed=12024217;
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                                                                                                                                                                                                             PRINTS; PR00624; HISTONEH5
                                                                                                                                                                                                                                       MBL; AE011948; AAM37903.1; -. InterPro; IPR005819; Histone_H5.
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155 AA;
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52.0%;
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Pred. No. 0.24
4; Mismatches
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DB 16;
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Query Match Best Local Similarity

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SEQUENCE
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Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
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                                                                                                                                                                                                                             Kaiser B., Kunkel W., Saluz H.P., Munder T.;
"Identification of Candida albicans protein domains with
transcriptional activating properties in Saccharomyces cerevisiae.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
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01-MAY-1999 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                             EMBL;
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Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
Uguda Y., Sugimoto S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterineae; Corynebacteriaceae;
NCBI_TaxID=152794;
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Pred. No. 0.22
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Pred. No. 0.28
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Q8WQ44;
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                                                                                                                                                                                                                                                            "Tapageorgiou F., Soteriadou K.;
"Identification of a Leishmania infantum gene
H1-like nuclear protein.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tzortzakis N., Papageorgiou F.T., Tzinia A.K., Soteriadou K "Identification and characterization of a novel Leishmania encoding for a putative histone H-1 like transcription fact Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ237814; CAD21431.1; -.

ENERGY PROCESS 19, Histone H5.
                                                                                                                                                                                                                           Nuclear protein.
SEQUENCE 111 AA;
                                                                                                                                                                                                                                                                                                                                           18 kDa nuclear protein.
Leishmania infantum.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
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01-JUN-2002
Bordetella pertussis
                      Histone
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Page 6
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Search completed: January 21, 2004, 09:00:26 Job time: 21.1169 secs
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-BPW28;

MEDLINE=95319329; PubMed=7596289;

SCARIATO V., Arico B., Goyard S., Ricci S., Manetti R., Prugnola A.,

Manetti R., Polverino-De-Laureto P., Ullmann A., Rappuoli R.;

"A novel chromatin-forming histone H1 homologue is encoded by a
dispensable and growth-regulated gene in Bordetella pertussis.";

Mol. Microbiol. 15:871-881(1995).

EMBL; L37438; AAB59120.1; -.

EMBL; L37438; AAB59120.1; -.
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Alcaligenaceae; Bordetella.
NCBI_TaxID=520;
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution.

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	AAG00755 AAG00759	21	218 218	35.4 4	75.5 75.5	41 42
	ABP62982	23	216	•	75.5	40
	ABP41465	23	201	٠	75.5	39
	ABP00299	23	111	•	75.5	38
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	AAY57358	21	226		77	36
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	AAY57331	21	222	•	77	ω 4
	AAY34033	20	222	•	77	ω u
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	AAY57366	21	158	•	77	31
	AAY34068	20	158	•	77	30
	AAY57364	21	116	36.2	77	29
	AAY34066	20	116	36.2	77	28
	AAY57365	21	103	36.2	77	27
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	ABB60086	22	2151	•	77.5	25
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	ABG71044	23	80	•	81	23
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	AAG70868	22	427		œ	21
	AAB20575	21	205	40.1		20
	ABJ18771	24	347	40.4		19
	AAW44936	19	198	40.4	86	18
	AAW43082	19	198	40.4	86	17
	AAW44934	19	39	0	86	16
	ABG28693	22	334	0	87	15
	AAY57353	21	214	N		14
	AAY34055	20	214		9	13
	AAY14928	20	223	42.7	91	12
	AAR06445	11		44.1	9	11
	ABB49123	23	239	44.4	94.5	10

ALIGNMENTS

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AAY82572;
                      AAY82572 standard; peptide; 45
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Copolymer molecular weight TV-marker amino acid sequence SEQ ID NO:2.

28-JUL-2000

(first

entry)

RAYBULT 1
AAY88251
ID AAY88
XX AAY88
XX AAY88
XX AAY88
XX COPC
XX OSTE
XX OSTE Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antinflammatory; antidiabetic; thyronimetic; haemostatic; antipporiatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; antianaemic; ocodition; multiple sclerosis; rheumatoid arthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; Gi Hashimoto's disease; Hashimoto's disease; idiopathic pemphigus vulgaris; systemic lup Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; lupus erythematosus. myxoedema; myasthenia gravis;

Unidentified.

WO200018794-A1

24-SEP-1999; 99WO-US22402.

06-APR-2000

25-SEP-1998; 98US-0101693.

(YEDA) YEDA RES & DEV CO LTD

(TEVA-)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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                                                                                          Unidentified.
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                                                                                                                                                                                    Crohn's disease; chronic immune thrombocytopaenia purpura; colitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKKYAKKAKAEKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                    molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45
                                                                                                                                                 disease; idiopathic myxoedema; myasthenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽,
                                                                                                                               systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 213; DB 21;
Pred. No. 1.6e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
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Hashimoto's disease; idiopathic myxoedema; myasthenia pemphigus vulgaris; systemic lupus erythematosus.

Unidentified

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RESULT 3
AAY82573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contributed by the present invention. The present convention describes polypeptides (I) for determining the molecular convention describes polypeptides (I) for determining the molecular convention and an amino acid composition corresponding to the copolymer. The copolymer copolymer (CP), which has an identified molecular weight can an amino acid composition corresponding to the copolymer. The copolymer acetate related tetrapolymers. The polypeptides may also be considered for treating and preventing immune diseases in a mammal. Autoimmune contibody-mediated diseases. Such diseases in clude arthritic conditions, contact sensitivity diseases include arthritions, e.g. multiple consensations, colitis, contact sensitivity disease, diabetes mellitus, draves conditions, colitis, contact sensitivity disease, diabetes mellitus, Graves contact sensitivity disease, diabetes mellitus, Graves concententinitis, crohn's disease, chronic immune thrombocytopaenia contact sensitivity disease, diabetes mellitus, Graves consensation, pemphigus vulgaris, or systemic concententinitis, austain agravis, psoriasis, pemphigus vulgaris, or systemic conclude host-versus-graft disease, graft-versus-host disease, and concenter weights and physical properties which are analogous to contact molecular weights and physical properties which are analogous to contact molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                             glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glatiramer acetate molecules, molecular weight markers.
                                                                          Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
                                                                                                                                                                                                                    Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                         Copolymer molecular weight TV-marker amino acid sequence SEQ ID
                                                                                                                                                                                                                                                                                                  28-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 AAY82573 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 14; 72pp; English.
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(TEVA-) TEVA PHARM USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.8%;
76.6%;
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Pred. No. 5.9e-08;
0; Mismatches 7
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RESULT 4
AXY8250
ID AAY8
XX AAY8
AC AAY8
XX AAY8
XX COpo
XX COpo
XX COpo
XX COpo
XX Opo
XX Opo
XX AAY8
AN Infil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
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                  glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis;
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                                                                                                                                                    Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                    Copolymer molecular weight TV-marker amino acid sequence SEQ ID
                                                                                                                                                                                                                                                      28-JUL-2000
                                                                                                                                                                                                                                                                                                         AAY82575
                                                                                                                                                                                                                                                                                                                                                         AAY82575 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weighte and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systlupus erythematosus. Mediated-mediated diseases which can be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-317499/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 14; 72pp;
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                                                                                                                                                                                                                                                         entry)
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68.4%;
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Pred. No. 7.2e-08;
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thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
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purpura;
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28-JUL-2000 AAY82576; AAY82576

(first entry)

standard; peptide; 86

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RESULT 5
AAY82576
ID AAY8
XX
AC AAY8
XX
DT 28-J
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                            antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or systemic lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      weight TV-marker polypeptides from the present invention. The present invention describes polypeptides (I) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
pemphigus vulgaris; systemic lupus erythematosus.
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(TEVA-) TEVA
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                                                                                                                                                                                                                                                                                                            Conservative
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PHARM USA INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                     markers.
                                                                                                                                                                                                                                                                                                                              61.5%;
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                                                                                                                                                                                                                                                                                                                              Score 131; DB 21;
Pred. No. 2.4e-07;
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                                                                                                                                                                                                                                                                                                                6,
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                                                                                                                                                                                                                                                                                                                                                    77;
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Copolymer; molecular weight marker; TV-marker; immune

Copolymer molecular weight

TV-marker amino acid

sequence

SEQ

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NO: 6

disease;

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                                                                                                                                                                                                                                                                                        cc weight TV-marker polypeptides from the present invention. The present cinvention describes polypeptides (1) for determining the molecular cc weight of a copolymer (CP), which has an identified molecular weight CC and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for CC glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune CC diseases which may be treated include either cell-mediated or creating diseases such diseases include arthritic conditions, cc antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple CC sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic anaemia, autoimmune oophoritis, autoimmune thyroiditis, autoimmune CC uncertinitis, Crohn's disease, chronic immune thromocytopaenia CC uncortinitis, Crohn's disease, chronic immune thromocytopaenia CC myxoedema, mysathemia gravis, psoriaeis, pemphigus vulgaris, or systemic CC include host-versus-graft disease, graft-versus-host disease, and celined molecular weights and physical properties which are analogous to CC delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to CC glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                        Query Match
Best Local Similarity
Matches 39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antityroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 10; Page 14; 72pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pemphigus vulgaris;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
61
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  YKAEAAKKAYKAEAAKAAAKEAAYEA
                                                                                                                   AKKYAKK-----AKAEKA-----KKAYKAAEAKKAAKYE------
                                                                              AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                            weight markers.
                                                                                                                                                                                                                                         98
                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0101693.
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                                     KAAAEKAAAKEAAYEA 45
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                                                                                                                                                                           59.4%;
45.3%;
                                                                                                                                                          0,
                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lupus erythematosus.
                                                                                                                                                          Mismatches
                                                                                                                                                    e 126.5; DB 21;
No. 8.3e-07;
No. 8.6-07;
86
                                                                                                                                                                                             21;
                                                                                                                                                          Indels
                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune diseases
                                                                                                                                                                                                 86;
                                                                                                                                                          41;
                                                                                                                                                          Gaps
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RESULT 6
AAY82574
CC AAY82571 to AAY82577 represent specifically claimed copolymer molecular CC weight TW-marker polypeptides from the present invention. The present CC invention describes polypeptides (I) for determining the molecular CC weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight and an amino acid composition corresponding to the copolymer. The CC and an amino acid composition corresponding to the copolymer. The CC used for treating and preventing immune diseases in a mammal. Autoimmune CC used for treating and preventing immune diseases in a mammal. Autoimmune CC diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, CC demyelinating diseases and inflammatory conditions, e.g. multiple CC elevates, autoimmune ophoritis, osteoarthritis, autoimmune hord commune cophoritis, cortact sensitivity disease, diabetes mellitus, Graves CC uveoretinitis, Crohn's disease, chronic immune thrombocytopaenia CC purpura, colitis, contact sensitivity disease, diabetes mellitus, Graves C disease, Guillain-Barre's syndrome, Hashmoto's disease, diopathic cupus erythematosus. Mediated-mediated diseases which can be treated contact sensitivity disease, diabetes mellitus, Graves C lupus erythematosus. Mediated-mediated diseases which can be treated contact disease and disease 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antianaemic; immunosuppressive; demyelinating disease; osteoarthritts; inflammatory condition; multiple sclerosis; rheumatoid arthritis; crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Gullain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                      include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipporiatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-317499/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copolymer molecular weight TV-marker amino acid sequence
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(TEVA-) TEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHARM USA INC.
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Query Match
Best Local Similarity 71.7
Matches 32; Conservative

56.6%;

Score 120.5; DB 2 Pred. No. 2.8e-06;

DB 21;

66; 7;

6

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Mismatches

Indels Length

Gaps

2

Sequence

6

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NO:1

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RESULT 7
AXV8251
ID MAY88
XX AXX8
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                                                         CC Weight TV-marker polypeptides from the present invention. The present convertion describes polypeptides (1) for determining the molecular convertion describes polypeptides (1) for determining the molecular weight of a copolymer (CP), which has an identified molecular weight convertion acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for conjugation acid composition corresponding to the copolymer. The copolymerides of the invention are used as molecular weight markers for conjugation of the copolymer. The conjugation of the copolymer of the copolymer of the copolymer. The copolymerides may also be used for treating and preventing immune diseases in a mammal. Autoimmune colleases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, e.g. multiple continating diseases and inflammatory conditions, e.g. multiple concentiation, autoimmune oophoritis, autoimmune thyroiditis, autoimmune haemolytic anaemia, autoimmune oophoritis, observathritis, autoimmune haemolytic conamina, autoimmune oophoritis, autoimmune thyroiditis, autoimmune collinates, collitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain, Barre's syndrome, Hashimoto's disease, idiopathic convertinitis, contact sensitivity disease, diabetes mellitus, Graves disease, Guillain agravis, psoridasis, pemphigus vulgaris, or systemic conditions of the convertion have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antithyvoid; antiinflammatory; antidiabetic; theyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 10; Page 14; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-317499/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (YEDA ) YEDA RES & DEV CO LTD. (TEVA-) TEVA PHARM USA INC.
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RESULT 8
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Best Local :
                                                                                                                                                     To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pREV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1994 US4651009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequence, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes incoding the following segments: YKK, ABK, KRA, KRA, YEA, ARA KEA, and AAA. The remainal alanine residue is left behind following CNBr cleavage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                        certain a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                             Producing genes encoding random polymers of aminoacid(s) - producing recombinant polypeptide(s) with biological and/or immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-FEB-1990;
17-FEB-1989;
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03-JAN-1991
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                                                                    encephalomyelitis. They are used to prevent, arx demyelinating disorder, e.g. multiple sclerosis. be used as additives to hair care products to co effects on damaged hair or as supplements for die
                                                                                                              fusion protein.

The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or
                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 12; 25pp; English
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Sequence
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                         n amino acids.
30 AAQ05664.
3d on 25-MAR-20
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                            25-MAR-2003
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(first entry)
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89US-0312541.
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                              correct PA field.)
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Pred. No. 3.4e-05;
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                                                                        diets deficient in
                                                                                                                arrest or control a

    They may also confer beneficial

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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycopeptide; mannose; mannosylated; glycosylated; mannose receptor; macrophages; monocytes; destroy; cytotoxicity; label; image; alter; macrophage processing of antigen; HMC restriction; inflammation; inflammatory diseases; macrophage secretory products; Crohn's disease; legionnaires disease; mononuclear phagocytes; HIV; AIDS; lysosomal storage diseases; Gaucher's disease; asthma; alveolar macrophages metastasis; systemic macrophages; deliver; antigenic peptides; prevent transplant rejection;
                      Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organ transplantation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High affinity macrophage mannose receptor ligand compound #9.
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23-MAR-1993
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28; Conservative
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(first entry)
                                          34
/note=
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antitumour
                                                                                                                                                                                                                                                                                                                                                                                            "opt may have mannose, fuce N-Ac-glucosamine. May also interfering substits."
"opt may have mannose, N-Ac-glucosamine."
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                               "opt may have mannose, N-Ac-glucosamine."
                                                               "opt may have mannose, N-Ac-glucosamine."
                                                                                                "opt may have mannose, N-Ac-glucosamine."
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                                                                                                                                                                N-Ac-glucosamine.
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                                                                                                                                                                          may have mannose,
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Pred. No. 0.00089;
4; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; toxins.
                                                                                                                                                                                                          fucose,
                                                                                                                                                                                                                                                                                                                                                                       fucose, glucose
           fucose, glucose or
                                                                                                          fucose, glucose
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RESULT 10 ABB49123

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ABB49123;

ABB49123 standard; Protein;

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8

Listeria 05-FEB-2002

monocytogenes protein #1827.

(first entry)

Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;

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This compound represents a glycopeptide effective in inhibiting the CC binding of labelled mannosylated BSA to mannose receptors. Mannose CC receptors are uniquely found on macrophages and not on monocytes, CC Glycopeptides such as this provide a mechanism to trayet macrophages. CC specifically, to image, label, destroy or otherwise alter their CC antigen processing function. In addition they can be conjugated to CC solid supports and used to purify mannose receptors from a variety CC of sources. They are useful in the treatment of inflammatory CC diseases driven by macrophage secretory products eg. Crohn's CC disease; infectious diseases in which macrophages harbour replicating CC infectious agents eg. Legionnaires disease; viral infections CC disease; in which macrophages harbour replicating CC diseases, in which macrophages are principally involved eg. CC diseases, in which macrophages are principally involved eg. CC diseases, in which macrophages are principally involved eg. CC diseases, as than mediated by alveolar macrophages. The peptides CC can also be used to deliver antigenic peptides as conjugates to a CC macrophage to marshal an immune response; also self peptides to CC prevent tissue transplant rejection.
                                                                                               Query Match
Best Local S
Matches 26
                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New high affinity mannose receptor ligand cpds. - for diseases mediated by macrophage activity e.g. asthma, inflammatory diseases and infectious diseases, e.g. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAY-1991;
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AAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAAKAA
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nilarity 63.4%;
Conservative
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                                                                                               Score 98; DB 13;
Pred. No. 0.00055;
L; Mismatches 14
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                                                                                                                                                  Length 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes—related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L.
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                     monocytogenes and related organisms.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P; Daniels J, Goebel W, Kreft J, Kuhn M, Ng B, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-García P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio B, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2001; 2001WO-FR01118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vitamin
Recombinant copolymer 1; COP-1-77;
                                                                                                                                                             AAR06445 standard; protein; 154
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; SEQ ID No 1828; 192pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                    KAAAEKAEADKKKQEEDAVKAANAKKEQEAAEEKAAADKAAAEKAAAE
                                                                                                                                                                                                                                                                                      239
                                   copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                         44.4%;
56.2%;
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Pred. No. 0.0072;
7; Mismatches
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 myelin basic
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 protein; MBP
                                                                                                                                                                                                                                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                            239;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      To improve the expression of rCOP-1 polypeptides in B. coli, genes coding for rCOP-1-77 were subcloned from pREV 2.1 to pBG3-ZdeltaN CC (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins CC consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences.

CC A methionine residue occurs between the Protein A and rCOP-1 sequences. Originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. TCC rCOP-1-77 contains oligonucleotide duplexes incoding the following Cr rCOP-1-77 contains oligonucleotide duplexes incoding the following CC rCOP-1-77 contains oligonucleotide duplexes incoding the following CC segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein.

CC segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the fusion protein.

CC enceptalomyelitis They are used to prevent, arrest or control a CC demyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial ceffects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Mycobacterium vaccae protein; antigen; T cell activation; cytokine; choritic cell maturation; infectious disease; immune disorder; cancidendritic rell maturation; infectious disease; immune disorder; cancidendratery system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunological activity; autoimmune encephalomyelitis;
multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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17-FEB-1989;
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                                                                                                                                                                                               Amino acid sequence of M. vaccae antigen GV-45.
                                                                                                                                                                                                                                                                  25-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                               AAY14928 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 11; 25pp;
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AAQ05665.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                  (first entry)
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89US-0312541.
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                                                                                                                                                                                                                                                                                                                                                                                               protein; 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                       AAY34055
                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides heat-killed Mycobacterium vaccae, or recombinant CC M. vaccae proteins. The M. vaccae protein may be employed to activate T cells and natural killer cells, to stimulate the production of CC cytckines, to enhance the expression of co-stimulatory molecules on CC dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant CC methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the CC treatment, prevention, and detection of disorders including infectious CC treatment, prevention, and detection of disorders including infectious CC treatment, prevential infections, asthma, allergies, tuberculosis, Such as mycobacterial infections, asthma, allergies, tuberculosis, CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as psoriasis, atopic dermatitis, eczema, allergic contact dermatitis, allegicia areata, and skin cancers such as basal carcinoma, squamous cell
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1997;
11-JUN-1998;
17-SEP-1998;
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23-DEC-1997;
23-DEC-1997;
                           Mycobacterium tuberculosis.
                                                    Ulcerative colitis; histone; H1-like antigen; porin antigen; Bacteroides antigen; inflammatory bowel disease; IBD; pANCA; perinuclear anti-neutrophil cytoplasmic antibody.
                                                                                                                  M. tuberculosis histone H1-like antigen.
                                                                                                                                                                            AAY34055
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 239; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enhancing immune response to an antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-430163/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prestidge RL,
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                                                                                                                                                                                                        AAY34055 standard; protein; 214 AA.
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                                                                                                                                                                                                                                                                                                           AKKYA-KKAKAEKAKKAYKAAEAKKAAKYEKAA-AEKAAAKEAAYEA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell
                                                                                                                                                                                                                                                                                                                                                                                                                                 and melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                      223
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                                                                                                                                            (first entry)
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98US-0095855.
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97US-0997080
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Pred. No.
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                                                                        diagnosis;
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WO9945955-A1.

Cohavy O,

Braun J;

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RESULT 14
AAY57353
ID AAY57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a method for the diagnosis, prevention and cc treatment of ulcerative coiltis (UC) using histone H1-like antigen, a CC porin antigen or a Bacteroides antigen as a target antigen. The novel cc method of diagnosing UC in a subject suspected of having inflammatory bowel disease (IBD) comprises: (1) obtaining a sample from the subject; CC (2) contacting the sample with a histone H1-like antigen, or perinuclear CC canti-neutrophil cytoplasmic antibody (pANCA)-reactive fragment, to form a CC complex of the histone H1-like antigen, or the pANCA-reactive fragment, and antibody to the histone H1-like antigen; and (3) detecting the CC presence or absence of the complex where the presence of the complex CC indicates that the subject has UC. The pANCA-reactive histone H1-like antigen, porin antigen and Bacteroides antigen are useful in the CC diagnosis, prevention and treatment of UC. The methods can also be used CC for identifying agents useful for treating UC. The present sequence CC represents a M. tuberculosis histone H1-like antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ulcerative colitis; inflammatory bowel disease; porin antigen; MAb; pANCA; perinuclear anti-neutrophil cytoplasmic antibody; 214 protein; histone H1; isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of histone H1, porin or Bacteroides antigens as targets for diagnosis, prevention and treatment of ulcerative colitis -
                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M. tuberculosis histone H1-like protein,
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                                                                                                                12-APR-1996;
11-APR-1997;
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                                                        (REGC ) UNIV CALIFORNIA
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l Similarity 55.6%;
25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        tuberculosis
                                                                                                                   96US-0057846.
97US-0837058.
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Pred. No. 0.02:
4; Mismatches
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Diagnosing ulcerative colitis or susceptibility, by detecting complex formation between microbial porin antigen and perinuclear anti-neutrophil cytoplasmic autoantibodies -

WPI; 2000-255695/22

Example 5; Fig 10; 49pp; English.

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a method for diagnosing ulcerative colitis in a subject suspected of having inflammatory bowel disease. The method comprises reacting a patient sample with a porin antigen that is immunologically reactive with pANCA (perinuclear anti-neutrophil cytoplasmic antibodies) and detecting formation of a Ag-pANCA complex as indicative of ulcerative colitis. The method is used to diagnose ulcerative colitis or susceptibility to it. The present sequence represents a histone H1-like protein of M. tuberculosis, designated 214.
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                            Claim 20; SEQ ID No 59052; 103pp; English.
                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                        WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                 31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #28684.
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                                                                                                                                                                                                                                                                       RT,
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2000US-0649167.
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                                                                                                                                                                                                                       CC (II) (II) is useful for generating antibodies against it, detecting or CC (III) (III) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polymuclectide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC diagnostic amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO
                                                                                  Matches
                                                                                                    Query Match
Best Local
                                                                                                                                                                 Sequence
                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences.
214 ARKKAATETAEKAKAQADKKAAAEKAAADKKAAAEKAATDKKAAEKA 260
                       L Similarity
27; Conserv
                                                                                                                                                                   334 AA;
                                                                                  Conservative
                                                                                                    40.8%;
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                                                                                                    Score 87; [
Pred. No. 0.
                                                                                  Mismatches
                                                                                                                       DB 22;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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213
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L: /cgn2_6/ptodata/2/pubpaa/US07
2: /cgn2_6/ptodata/2/pubpaa/PCT_1
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_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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NEW PUB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11111111111111111111111111111111111111	Result No.
213 138 134.5 131.5 126.5 120.5 120.5 120.6 91 91 91 89.5 85 85 87	Score
100.0 634.8 631.1 59.4 500.4 422.7 422.7 422.7 422.7 422.7 422.7 422.7 6.66.66.66.66.66.66.66.66.66.66.66.66.6	Query Match 1
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Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 6, Appli Sequence 1, Appli Sequence 20, Appl Sequence 201, Appl Sequence 201, Appl Sequence 201, Appl Sequence 120, Appl Sequence 189, Appl Sequence 5751, Appl Sequence 5751, Apple Sequence 12370, Apple Sequence 12370, Apple Sequence 24, Apple Sequence 24	Description

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sequence 13000, A				>		Sequence 11652, A			00		Sequence 17058, A		Sequence 4, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 12155, A		23		Sequence 559, App	Sequence 2, Appli	Sequence 2597, Ap	Sequence 32, Appl		Sequence 40, Appl	(L)	Sequence 39, Appl	109

ALIGNMENTS

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RESULT 2
US-09-816-989A-7
; Sequence 7, Application US/09816989A
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                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOPTWARE: Patentin version 3.1
SEQ ID NO 2
                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 45; Conserv
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                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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llarity 100.0%;
Conservative 0
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Pred. No. 1.4e-16;
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Best Local S
Matches 39
                  Sequence 5, Application US/09816989A Patent No. US20020115103A1 GENERAL INFORMATION:
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Matches
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TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
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PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR FILING DATE: 1998-09-25 PRIOR APPLICATION NUMBER: FCT/US99/22402 PRIOR FILING DATE: 1999-09-24
APPLICANT: Gad,
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TYPE: PRT
ORGANISM: Artificial Sequence
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76.6%;
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Pred. No. 5.66
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Pred. No. 4.8e-08;
0; Mismatches 7
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CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT PILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 77
TYPE: PRT
ORGANISM: Artificial Sequence
PAGRANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial
US-09-816-989A-5
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Matches
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Best Local Similarity
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Best Local Similarity
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Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT PAPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR APPLICATION NUMBER: FOT/US99/22402
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 7
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US
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                                                                                                                                                                                                                                                                                             LENGTH: 86
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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                                                                              AKKYAKKEKAYAKKAEKAAKKAEAKAYKAAEAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lis, Doris
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                           59.4%;
45.3%;
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50.6%;
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Pred. No. 1.9e-07;
0; Mismatches 6
                                                                                                                                                                             Score 126.5; DB 1
Pred. No. 6.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Artificial Sequence: Synthetic Peptide
                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
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US-10-205-979-52
; Sequence 52, Application US/10205979
; Publication No. US20030147861A1
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                                                                                                                                       RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-816-989A-1
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US-09-816-989A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-816-989A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Appraise Sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOPTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lis, Doris
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR PILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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EQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lie, Dorie
TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
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TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
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                                                                                                                                                                                                                                                                                                                                            АККҮАККАКАЕКАККАҮКААЕАККААКҮЕКАААЕКАААКЕААҮЕА 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09816989A
                                                                                                                                                                                                                                                              AKKYAKKEKA--AKKAYK-----KEAKAKAAEAAAKEAAYEA 35
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llarity 71.1%;
Conservative
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Pred. No. 2.5e-05;
1; Mismatches 5;
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Pred. No. 2.2e-06;
0; Mismatches 6;
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US-10-229-567-27, Application US/10229567; Sequence 27, Application US/10229567; Publication No. US20030092080A1; GENERAL INFORMATION:
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; ORGANISM: Mycobacterium vaccae
US-10-205-979-52
                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-051-643-201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 201
LENGTH: 223
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 52
LENGTH: 223
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CURRENT APPLICATION NUMBER: US/10/205,979
CURRENT FILING DATE: 2002-07-25
ERIOR APPLICATION NUMBER: 60/308,446
PRIOR FILING DATE: 2001-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: US 08/996,624
PRIOR FILING DATE: 1997-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of
TITLE OF INVENTION: System using Mycobacterium Vaccae
FILE REFERENCE: 11000.1008c2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Watson, James D. APPLICANT: Tan, Paul L. J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 21
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mycobacterium vaccae
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NUMBER OF SEQUENCES:
                                                            TITLE OF INVENTION:
                                                                                                  APPLICANT: Braun, Jonathan
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                                                                                                                                                                                                                                                             137 AKKAATKAAPAKKATAAKKAAPAKKATAAKKAAPAKKAPAKKAATKA 183
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                                                                                                                                                                                                                                                                                                                                                                Similarity
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59.6%;
                                                                                                                                                                                                                                                                                                                                                              42.7%;
                                                                                 Offer
                                     Diagnosis, Prevention and Treatment of Ulcerative Colitis, and Clinical Subtypes Thereof, Using
                    Microbial UC pANCA antigens
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Pred. No. 0.013;
5; Mismatches
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Pred. No. 0.013;
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                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 223;
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CORRESPONDENCE ADDRESS

ADDRESSEE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700

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; SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-229-567-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-127-032-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
  Query Match
                                         ORGANISM: Pseudomonas aeruginosa -10-127-032-120
                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 120, Application US/10127032
Publication No. US20030113742A1
                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/285,190
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: US 60/344,142
PRIOR FILING DATE: 2001-10-24
                                                                                                                                                                                                                                                                                                               APPLICANT: Greenberg, Everett Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION OF
TITLE OF INVENTION: BIOFILM FORMATION
FILE REPERENCE: UIZ-070CP
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/127,032
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                     TYPE: PRT
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                                                                                                      ENGTH: 347
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APPLICATION NUMBER: US/09/417,264
PILING DATE: <Unknown>
APPLICATION NUMBER: US 09/041,889
PILING DATE: <Unknown>
APPLICATION NUMBER: US 09/041,889
ATTORNEY/ACENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TERENCOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 АККУАККАКАЕКАККАУКААЕАККААКУЕКАААЕКАААКЕААУЕА 45
                                                                                                                                                                                                                                                                                                                                                                              Bangera, M. Gita
Lory, Stephen
Greenber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 214 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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55.6%;
  40.4%; Score 86;
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  DB 15;
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Length 347;
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US-10-156-761-9889
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US-09-738-626-5751
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SOFTWARE: Pate
SEQ ID NO 5751
LENGTH: 165
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SEQ ID NO 9889
LENGTH: 376
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5751, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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Publication No.
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                                                PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UF 2001-204089
PRIOR FILING DATE: 2001-05-30
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US/99/377484
PRIOR FILING DATE: 1999-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                     PRIOR APPLICATION NUMBER: JP 00/159162 PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAKAGAWA, SATOSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 39.9%;
Local Similarity 50.0%;
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YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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HORIKAWA, HIROSHI
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SAKAKI, YOSHIYUKI
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o. US20030119018A1
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Pred. No. 0.1;
6; Mismatches
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RESULT 15
US-09-820-843A-24
US-09-820-843A-24; Sequence 24, Application US/09820843A; Publication No. US20030039963A1; GENERAL INFORMATION:
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US-10-156-761-12370
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US-09-820-843A-24
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12370
LENGTH: 272
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Best Local Similarity 46.3%; Pred. No. 0.41;
Matches 19; Conservative 7; Mismatches 15; Indels
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                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0 SEQ ID NO 24
                                                                                                                                                                                                                                         APPLICANT: COUNCIL OF Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEI
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: Q63915
CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
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APPLICANT:
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CURRENT FILING DATE: 2002-05-29
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30
  TENGTH: 309
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: polyhydroxyalkanoate synthesis protein PhaF
NAME/KEY: misc_feature
OTHER INFORMATION: gi|9951352
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APPLICANT: IKEDA, HARUO
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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SAKAKI, YOSHIYUKI
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      Query Match
      36.6%; Score 78; DB 11; Length 309;

      Best Local Similarity 54.8%; Pred. No. 0.47;
      9red. No. 0.47;

      Matches 23; Conservative 0; Mismatches 19; Indels 0; Gaps

      Qy
      1 AKKYAKKAKAKKAYKAAEAKKAAKYEKAAAEKAAAKEAA 42

      Qy
      1 AKKYAKKAKAKAKAYKAAEKAAKPAAKPAAKPAAKPAA 183

      Db
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Search completed: January 21, 2004, 09:10:08 Job time : 16.3636 secs

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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR
FILE REFERENCE: 60807-A
                                                                            TYPE: PRT
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	26, 1	14, A	15, App	3, Appl	11, App	10, A	13, A	11, Appl	10, A	11, Appl	•	47, App	22853,	4, Appl	16, App	2, Appl	13, App	-

ALIGNMENTS

WEIGHT MARKERS

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Sequence 7, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 45
TYPE: PRT
                                                                                          CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 109
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Best Local Similarity
                                      ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: PEPTIDE
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OTHER INFORMATION:
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Pred. No. 1.2e-16;
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LENGTH: 56
TYPE: PRT
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CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 5
LENGTH: 77
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APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
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Best Local Similarity
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
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TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                   LENGTH: 77
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 2.9e-08;
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Pred. No. 1.1e-07;
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Pred. No. 3.5e-08;
0; Mismatches 5
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RESULT 7
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US-09-405-743A-4
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US-09-405-743A-4
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COTHER INFORMATION: Description; OTHER INFORMATION: PEPTIDE
US-09-405-743A-6
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US-09-405-743A-6
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Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIKAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
SEQ ID NO 4
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LENGTH: 86
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Best Local
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Best Local Similarity 45.3%;
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                              1 АККУАККАКАЕКАККАУКААЕАККААКҮЕКАААЕКАААКЕААҮЕА 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AKKYAKK-----AKAEKA-----KKAYKAAEAKKAAKYE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKAEAAKKAYKAEAAKAAAKEAAYEA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KAAAEKAAAKEAAYEA 45
                                                                                                                                                                             AKKYAKAAKAE--KKEYAAAEAK----YKAEAAKAAAKEAAYEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKKYAKKEKAYAKKAEKAAKKAEAKAYKAABAKKKAKAEAKKYAKAAKAEKKEYAAAEAK 60
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description of Artificial Sequence: PEPTIDE
                                                                                                                                                                                                                                                                                                                                         Description of Artificial Sequence: PEPTIDE
                                                                                                                                                                                                                                                                  56.6%;
71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                   Score 120.5; DB 4
Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 126.5; DB of Pred. No. 3.8e-07, O; Mismatches
                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                     σ,
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                                                                                                                                                                                                                                                                                        66,
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RESULT 8
US-09-095-855-201
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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
LENGTH: 35
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                   NAME: Sleath, Janet REGISTRATION NUMBER: 37,007 REFERENCE/DOCKET NUMBER: 110 TELECOMMUNICATION INFORMATION: TELEPHONE: 206.269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
MOLECULE TYPE:
                                                                                                                                                                                                                                                           FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Compounds and TITLE OF INVENTION: Treatment and
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                 TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                  TOPOLOGY:
                                                                                                                                                          TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201, Application US/09095855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.7%;
Similarity 64.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seattle
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                                                                                     223 amino acids
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                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
                protein
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                                             single
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                                                                                                                        201:
                                                                                                                                                                                                             11000.1002c3

    Mismatches

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Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methods for Diagnosis of Mycobacterial Infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 35;
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US-09-041-889-27
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EARLIER APPLICATION NUMBER: 08/705,347
EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 201
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 42.7
Best Local Similarity 59.6
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6033864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 640670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/873,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 09/095,855
EARLIER FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Watson, James D.
APPLICANT: Tan, Paul I. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
FILE REFERENCE: 11000.1002c4
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Mycobacterium vaccae
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopyy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/041,889
FILING DATE:
                                                                                                                                                                                                                                                                                                                        APPLICANT: Braun, Jonathan APPLICANT: Cohavy, Offer TITLE OF INVENTION: Diagnos TITLE OF INVENTION: Ulcerat TITLE OF INVENTION: Microbi
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   CITY: San Diego
STATE: California
                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 AKKAATKAAPAKKATAAKKAAPAKKATAAKKAAPAKKAPAKKAATKA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 АККҮА-ККАКАЕКАККАҮКААЕАККЛАКҮЕКАА-АЕКАААКЕЛАҮЕА 45
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                                                                                                                                                                                                                                           3E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09205426
                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                        Microbial UC pANCA antigens
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Pred. No. 0.0062;
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Pred. No. 0.0062;
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                                                                  #1.25
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CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

US 08/837,058

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RESULT 11
US-09-417-264-27
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; MOLECULE TYPE: US-09-417-264-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                                    NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
TOPOLOGY: lina
VOLECUT n
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OP INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colltis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC panCA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: P-PM 3006
                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
STATE: California
                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                  (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.0%; ilarity 55.6%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
                                                                                                                                                      (619) 535-9001
                  peptide
                                                                                                                                                                                                                                                                                             US 09/041,889
                                                                                                                                                                                                                                                                                                                                                                         US/09/417,264
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US-09-252-991A-32957
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US-09-252-991A-29581
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                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SEQ ID NO 29581
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SEQ ID NO 32957
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Best Local Similarity 51.1
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 107196.130
FILE REFERENCE: 107196.130
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PTILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32957,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                  LENGTH: 316
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 407
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Local Similarity 55.6%;
hes 25; Conservative
                                                                                             Local
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                                 1 АККУАККАККАККАУКАЛЕАККАЛКУЕКАЛАЕКАЛАКЕЛА 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
AKKVAKKAPAKKATKAAKKAATKAPA---RKAATKAPAKKAATKA 152
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                             36.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.48;
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                                                                          Score 78; DB 4; Length 316; Pred. No. 0.22; 0; Mismatches 19; Indels
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RESULT 14 US-09-107-532A-5094

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US-09-041-889-39
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                                                                               Sequence 39, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC pANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5094, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5094
SEQUENCE CHARACTERISTICS:
                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/055,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/51571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION:
TELEPHONE: (781)893-5007
  ADDRESSEE:
STREET: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 53.7 es 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...700
SEQUENCE DESCRIPTION: SEQ ID NO: 5094:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 700 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
3E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                            36.4%; Score 77.5; DB 4; Length 700; 53.7%; Pred. No. 0.55; ative 7; Mismatches 9; Indels
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AND AMINO ACID SEQUENCES RELATING TO
FARCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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US-09-041-889-39
                                                                   Matches
                                                                                   Query Match
Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/837
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                        LENGTH:
51
                               amino acids
AKPKAKKAGAAKAKKPAGATPKKAKKAAGAKKAVKKTPKKAKKPAA 96
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                                                                 Conservative
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52.2%;
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                                                                                   Score 77; DB 3;
Pred. No. 0.088;
                                                                   Mismatches
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                                                                                                     DB 3;
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Search completed: January 21, 2004, 09:02:20 Job time: 8.47403 secs

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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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ALIGNMENTS

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Qy 1 Db 120 Qy 56 Db 178	A; Gene: COAA A; Map position: 17 min A; Start codon: GTG C; Keywords: nucleotide binding; P. F; 14-34/Domain: transmembrane #starts F; 78-301/Domain: helical #status; F; 355-362/Region: nucleotide-bindi Guery Match Best Local Similarity 53.0%; Matches 61; Conservative 11		RESULT 1 JV0057 tolA protein - Escherichia coli (strain K-12) C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text C;Accession: JV0057; B64810 R;Levengood, S.K.; Webster, R.E. R;Levengood, S.K.; Webster, R.E. A;Title: Nucleotide sequences of the tolA and tolB genes A;Title: Nucleotide sequences of the tolA and tolB genes A;Reference number: JV0057; MUID:90078104; PMID:2687247 A;Molecule type: DNA A;Residues: 1-421 <lev< td=""></lev<>
AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAK-EAAK 55 :: :	P-loop; transmembrane protein tatus predicted <mss> predicted <hsr> iding motif A (P-loop) Score 189.5; DB 2; Length 421; Pred. No. 1.6e-05; Pred. No. 1.6e-05; Il; Mismatches 32; Indels 11; Gaps 5;</hsr></mss>	A;Experimental source: strain JMI05 A;Rose: the authors translated the initiation codon GTG for residue 1 as Val A;Rose: D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Fitle: The complete genome sequence of Escherichia coli K-12. A;Ference number: A64720; MUID:97426617; PMID:9278503 A;Accession: B64810 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Rose: 1-421 <blat> A;Comment: 1-421 <blat> A;Experimental source: strain K-12, substrain MG1655 C;Comment: tolA and tolB proteins are necessary for collcins E2, E3, A, and K to reach to C;Genetics:</blat></blat>	RESULT 1 JV0057 TCJA protein - Escherichia coli (strain K-12) C;Species: Escherichia coli C;Species: Escherichia coli C;Accession: JV0057; B64810 R;Levengood, S:K.; Webster, R.E. J. Bacteriol. 171, 6600-6609, 1989 A;Title: Nucleotide sequences of the tolA and tolB genes and localization of their produ A;Reference number: JV0057; MUID:90078104; PMID:2687247 A;Accession: JV0057 A;Molecule type: DNA A;Residues: 1-421 < LEV> A;Residues: 1-421 < LEV> A;Residues: 1-421 < LEV>

RESULT F90725

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A;Cross-references: GB:BA000007; PIDN:BAB34197.1; PID:g13360233; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90725
                       histone H1 - sea urchin (Lytechinus pictus)
C;Species: Lytechinus pictus (painted urchin)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988
C;Accession: A25550
R;Knowles, J.A.; Childs, G.J.
Nucleic Acids Res. 14, 8121-8133, 1986
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A25550
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85576
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change
C;Accession: G85576
C;Accession: G85676
C;Accession: G
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A; Title: Comparison of the late H1 histone
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Pred. No. 4.7e-05;
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K.; Apodaca
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                                    A;Status: preliminary A;Molecule type: DNA
   ;Molecule type: DNA
;Residues: 1-376 <PAR>
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C; Accession: E83545
C; Accession: E83545
R; Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
adman, S.; Olson, M.V.
S:; Moule, S:; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C:; Quail, M:; Rutherford, K:; Simmonds, M:;

A;Title: Complete genome sequence of a multiple drug resistant

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AG0592
                                                                                                                                            tolA protein [imported] - Salmonella enterica subsp. enterica serovar C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov C;Accession: AG0592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:X04488; NID:g9616; PIDN:CAA28177.1; PID:g9617 C;Superfamily: histone H1 C;Keywords: chromosomal protein; DNA binding; nucleosome; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A25550; MUID:87040778; PMID:3022245
A;Accession: A25550
A;Molecule type: DNA
A;Residues: 1-210 <KNO>
                                                                                                                                                                                                                                         RESULT 6
AG0592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE004530; GB:AE004091; NID:g9946865; PIDN:AAG04360.1; A;Experimental source: strain PAO1
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A;Molecule type: DNA
A;Residues: 1-347 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: Complete genome sequence of Pseudomonas aeruginosa A,Reference number: A82950; MUID:20437337; PMID:10984043 A,Recession: E83525
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                                                                                                                                  R;Parkhill, J.; Dougan, G.;
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L.L.; (
                                                                                                                                 James,
                                                                                                                nes, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Cl
A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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Pred. No. 6.2e-05;
7; Mismatches 29;
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Pred. No. 3.2e-05;
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TolA colicin import membrane protein [imported] - Yersinia pestis (strain CO92) (;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AC0138
R;Parkhill, J: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, S23-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0138
                                                                                                                                                               mst101-1 protein - fruit fly (Drosophila hydei) (;Species: Drosophila hydei) C;Species: Drosophila hydei C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 C;Accession: S34153 R;Neesen, J; Heinlein, U.A.O.; Buenemann, H. submitted to the EMBL Data Library, June 1993 A;Reference number: S34153 A;Reference number: S34153 A;Recession: S34153
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A;Gene: STY0793
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  A; Cross-references:
C; Superfamily: neuro
                                                                                                        A; Molecule type: mRNA
A; Residues: 1-344 < NEE>
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A; Residues: 1-388 < KUR>
                                          C;Genetics:
A;Gene: FlyBase:Dhyd/mst101
                                                                                 A; Cross-references: EMBL: X73480; NID: g313199; PID: g313200
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nces: FlyBase:FBgn0011816 neurofilament triplet H p
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Pred. No. 7.8e-05;
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histone H1-beta, embryonic - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 23-Feb-1997
C;Accession: A28100
R;Lai, Z.C.; Childs, G.
Mol. Cell. Biol. 8, 1842-1844, 1988
A;Title: Characterization of the structure and transcriptional patterns of the A;Reference number: A28100; MUID:88246461; PMID:2837660
A;Accession: A28100
A;Acce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Neesen, J.; Padmanabhan, S.; Buenemann, H.
Eur. J. Biochem. 225, 1089-1095, 1994
A;Title: Tandemly arranged repeats of a novel highly charged 16-amino-acid motif represe lipha-helical rods within the extremely elongated spermatozoa of Drosophila hydel.
A;Reference number: S51364; MUID:95045538; PMID:7957199
A;Accession: S51364
                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-163,'E',164-236,'Q',237-254,257-320,'E',321-1390
A;Cross-references: EMBL:X73481; NID:g313201; PID:g313202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sperm tail-specific protein mst101(2) - fruit fly (Drosophila hydei)
C;Species: Drosophila hydei
C;Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S51364; S34154
                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S34153
A; Accession: S34154
                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Neesen, J.; Heinlein, U.A.O.; Buenemann, submitted to the EMBL Data Library, June 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-1390 <NEE>
A;Cross-references: EMBL:X73481
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                                                                                                                                             A;Cross-references: FlyBase:FBgn0011816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence
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Best Local S
Matches 58
                                                                                                                                                                                   ;Gene: mst101(2)
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                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAABAKK-AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKKCAEAAKKEKEAAEKKK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPAAKKAKKPAAKKAAKKPAAKKPAAKKAAAKPAPAKKAAKKPAAKKAAKKVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYAKKAE-KAYAKKAK--AAKEKKAYAKKEAKAYKAABAK-KKAKAEAKKYAKEAAK---
33.0%;
ilarity 46.2%;
Conservative 1
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48.7%;
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   Score 171.5; DB 2
Pred. No. 0.00051;
1; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 175.5; DB Pred. No. 0.0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 172.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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1993
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                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
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                                                                      Length 1390;
           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
           15;
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R;Kappe, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H. Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998
A;Title: A family of chimeric erythrocyte binding proteins of mala A;Reference number: Z16577; MUID:98115903; PMID:9448314
A;Accession: T09127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable erythrocyte-binding protein MABBL - Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: T09127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 histone H1, gonadal - sea urchin (Parechinus angulosus)
C;Species: Parechinus angulosus (angulate urchin)
C;Date: 31-Mar-1980 #sequence revision 31-Mar-1980 #text_change 16-Feb-1997
C;Accession: A91090; A91091; A02586
R;Strickland, W.N.; Strickland, M.; de Groot, P.C.; von Holt, C.; Wittmann-Liebold, Eur. J. Biochem. 104, 559-566, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus rminal cyanogen bromide peptides.
A;Reference number: A91090; MUID:80156831; PMID:6767609
A;Contents: sequence of residues 1-84
                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-1701 <KAP>
A;Cross-references: EMBL:AF031886; NID:g2947227;
A;Experimental source: subspecies yoelii; strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
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A;Note: 144-Arg was also found
C;Superfamily: histone H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 1-248 <STR>
A;Residues: 1-248 <STR>
A;Residues: 1-248 <STR>
R;Strickland, W.N.; Strickland, M.; Brandt, W.F.; von Holt, C.; Lehmann, A.; Wittmann-Li
Eur. J. Biochem. 104, 567-578, 1980
Eur. J. Biochem. 104, 567-578, 1980
A;Title: The primary structure of histone H1 from sperm of the sea urchin Parechinus and
A;Reference number: A91091; MUID:80156832; PMID:7363905
A;Accession: A91091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A91090
     Best Loc
Matches
                                                                                                              ;Introns: 62/1; 1648/1; 1674/2; 1697/1; Keywords: alternative splicing; cell
                                                                                                                                                                       Gene: maebl
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                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA binding; nucleosome; sperm
     Similarity 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KA--EAKKYAK-----AAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKAKKTSAAAKAKKAKAAAAKKAKAKAAAKRKAALAKKKAAAAKRKAAAKAKKAKKPKK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAAKKAKKPAKKSPKKAKKPAKKSPKKKKAKRSPKKAKKAAGKRKPAAKKARR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CEEAAKREKEA--AEKKKCAEAAKKEKE--ATEKQKCAEAAKKEKEAAEKKKCAEAA 1179
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                                                                                                            splicing;
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32.9%; Score 170.5; DB 2; 53.5%; Pred. No. 0.00068; Itive 11; Mismatches 31;
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                                                                                                      cell binding; erythrocyte invasion
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Pred. No. 0.00017;
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histone H1 - Chlamydomonas reinhardtii
(;Species: Chlamydomonas reinhardtii
(;Species: Chlamydomonas reinhardtii
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 23-Jul-1999
C;Accession: S59589; S62122
C;Accession: S59589; S62122
R;Fabry, S.; Mueller, K.; Lindauer, A.; Park, P.B.; Cornelius, T.; Schmitt, R.
Curr. Genet. 28, 333-345, 1995
Curr. The organization structure and regulatory elements of Chlamydomonas histone
A;Reference number: S59581; MUID:96120862; PMID:8590479
A;Accession: S59589
                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U16726
A;Note: the authors did not translate the codon for residue 1
R;Fabry, S.; Ford, C.; Lindauer, A.; Mueller, K.; Cornelius, submitted to the EMBL Data Library, October 1994
A;Description: The organization, structure and controlling elapses of the submitted to the SA;Reference number: 862122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A28456
R;Coles, L.S.; Robins, A.J.; Madley, L.K.; Wells, J.R.E.
J. Biol. Chem. 262, 9656-9663, 1987
A;Title: Characterization of the chicken histone H1 gene complement.
A;Reference number: A92655; MUID:87250632; PMID:3597432
A;Accession: A28456
                                                                                                                   A;Introns: 62/3; 101/3
C;Superfamily: histone H1
                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-173,'P',174-231 <FAW>
A;Cross-references: EMBL:U16726; NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-231 < FAB>
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C;Superfamily: histone H1
C;Keywords: acetylated amino end; chromosomal protein; DNA binding; nucleosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Gallus gallus (chicken)
C;Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 04-Mar-2000
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                                                                                                   C; Keywords: chromosomal protein; DNA binding; nucleosome
                                                                                                                                                                                                                                                                             A; Accession: S62122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-220 < COL>
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Best Local S
Matches 52
Best Loc
Matches
                  Match 31.7%;
Local Similarity 45.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEAYKA- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKKPGEVKEKAPRKRTPAAKPKKPAAKKPASAAKKPKKAAAAKKSPKKAKKPAAAATKKA
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10; Mismatches
                                                                                                                                                                                                 NID:g571479; PIDN:AAA98452.1; PID:g571480
                          Score 164.5;
Pred. No. 0.0
                            0.00038
                                                                                                                                                                                                                                                                                                                               controlling elements of Chlamydomonas
                                                 DB 2;
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  39;
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B, T.; Schmitt,
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RESULT 15
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Search completed: January 21, 2004, 09:01:40 Job time: 20.8182 secs
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C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: S19113; S14466
R;Wakarchuk, W.W.; Mueller, F.W.; Beck, C.F.
Plant Mol. Biol. 18, 143-146, 1992
A;Title: Two GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangements A;Reference number: S19113; MUID:92119224; PMID:1731966
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A;Molecule type: DNA
A;Residues: 1-265 <WAX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.6%; Score 164; DB 2; Length 265; Best Local Similarity 39.4%; Pred. No. 0.00045; Matches 50; Conservative 21; Mismatches 38; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: EMBL:X17208; NID:g18136; PIDN:CAA35080.1; PID:g18137;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 SA 221
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                                                                                                                                                                                                                                199 EAKAKEA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 RVAAEARAAAAAEARAAAAEAAAAAKARVAAEARAAAAAEARAAAAAEAAAAAKARAAA 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AKKYAKKAEKA------YAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEA 46 |: ||:|::| :: | |: | :: | 1: | :: | 1: | :: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1: | 1:
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MEDLINE=97133271; PubMed=8978668; Derouiche R., Gavioli M., Benedetti H., Prilipov A., Lazdunski C.,	INTERACTION WITH PORINS.	[5]	Proc. Natl. Acad. Sci. U.S.A. 88:5939-5943(1991).	"TOTA: a membrane process sivorved as	Levengood S.K., Beyer W.F. Or., Webbier K.E.;	MEDLINE=91296736; PubMed=2068069;	DOMAINS.	[4]	DNA Res. 3:137-155(1996).	corresponding to the 12.7-28.0 min region on the link	"A 718-kb DNA sequence of the Escherichia coli K	Yano M., Horiuchi T.;	Sampei G., Seki Y., Taqami H., Takemoto K., Wada C., Yamamoto Y.,	Mori H. Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito	Timing a Kitagawa M Makino K Magnida a Miki T Mizobichi K	Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,	MEDLINE=97061202; PubMed=8905232;	STRAIN=K12;		[3]	"The complete genome sequence of ascherichta cost N-14.	man B., Shao Y.;	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burlan	MEDLINE=97426617; PubMed=9278503;	STRAIN=K1	SEQUENCE FROM N.A.		Escherichia coli.";	their products, components of a multistep translo	"Nucleotide sequences of the tolk and tolB genes and localizati	Levengood S.K., Webster R.E.:	MEDLINE=9007	OBECONNEL TRIOS.	[1]		Enterobacteriaceae; Escher	Bacteria; Proteobacteria; Gamm	Escherichia coli.	TOLA OR CIM OR EXCC OR LKY OR B0739.	28-F1	01-FEB-1991 (Rel. 17, Last sequence update)	01-FEB-1991 (Rel. 17, Created)	P19934:	LA ECOLI TOLA ECOLI STANDARD: PRT	_

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lubkowski J., Hennecke F., Plueckthun A., Wlodawer A., "Filamentous phage infection: crystal structure of 93p with its coreceptor, the C-terminal domain of TolA.", Structure 7:711-722(1999).
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M28232; AAA24683.1; -.
EMBL; AE000177; AAC73833.1;
EMBL; D90713; BAA35405.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lloubes R.; "TolA central domain interacts with Escherichia coli porins."; EMBO J. 15:6408-6415(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS)
MEDLINE=99332679; PubMed=10404600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Inner
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; JV0057; JV0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fransport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EcoGene;
             _LYTPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF GROUP COLICINS (COLICINS A, E1, E2, E3, AND K). NECESSARY FOR THE COLICINS TO REACH THEIR RESPECTIVE TARGETS AFTER INITIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
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                                                                          178
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                                                                                                                                                    μ
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                                                                                                                                                    AKKYAKKAE----KAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAK-EAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EG11007; tolA.
                                                                          AAAEAOKKAEAAAALKKKAEAAEAAAAEARKKAATEAAEKAKAEAEKKAAAEKA
                                                                                                                           AEEAAKQAELKOKQAEEAAAKAAADAKAKAEADAKA--AEEAAKKAAADAKKKAEAEAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein transport;
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                                                                                                                                                                                                                              421 AA;
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        r membrane;
1 13
14 34
35 421
48 310.
311 421
224 278
              STANDARD
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                                                                                                                                                                                                                                                    351
351
351
350
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369
397
397
                                                                                                                                                                                                                              43156 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3D-structure;
                                                                                                                                                                          11; Mismatches
                                                                                                                                                                                       Score 189.5; DB 1
Pred. No. 4.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                       PERIPLASMIC (POTENTIAL).

DOMAIN II (ALDHA-HELICAL).

DOMAIN III (FUNCTIONAL).

10 X TANDEM REPEATS OF [ED]-K(1,2)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ructure; Complete proteon CYTOPLASMIC (POTENTIAL).
              PRT;
                                                                                                                                                                                                                             8B2F52B4B97C655E CRC64;
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              210
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RESULT
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Matches 58
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01-JAN-1988 (Rel.
15-JUL-1999 (Rel.
Late histone H1.
                                                                                                                                                                                                                                                                                                                 TOLA_PSEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lytechinus pictus and Strongelocentrotus purpuratus.";
Nucleic Acids Res. 14:8121-8133(1986)
-1- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                     SEQUENCE FROM N.A. STRAIN=PAO;
                                                                                                                                                                            Tola protein.
TOLA OR PA0971.
                                                                                                                                                                                                                                                                      P50600;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosomal
SEQUENCE :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restitute the succession of the succession
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Eukaryota; Metazoa; Echinodermata; Eleu
MEDLINE=97113525; PubMed=8955385;
                                                                                                                                  Bacteria; Proteobacteria;
                                                                                                                                                         Pseudomonas aeruginosa
                                                                                                                                                                                                                         16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR005818; Histone H1/H5
InterPro, IPR005819; Histone H5.
InterPro, IPR003216; Linkerhist N.
Pfam; PF00538; linker histone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A25550; A25550.
HSSP; P02259; 1HST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87040778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7653;
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                                                                                  NCBI_TaxID=287;
                                                                                                          Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lytechinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                  155
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an email to license@isb-sib.ch)
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(Rel.
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210 AA; 21746 MW; 08C38F64894007E2 CRC64;
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                                                                                                               Pseudomonas
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                                                                                                                                  Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 181; DB 1;
Pred. No. 9.3e-06;
8; Mismatches 36
                                                                                                                                                                                                                                                                                                                     PRT;
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a; Temnopleuroida; Toxopneustidae;
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                                                                                                                                                                                                                                                                                                                     347
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                                                                                                                                      Pseudomonadales;
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Matches 54; Conser
                                                                                                                                                                                 Q08695;
01-FEB-1995
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DOMAIN
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                      Drosophila hydei (Fruit fly)
                                                                                         Axoneme-associated MST101(1).
                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                    MST1
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TIGRFAMs; TIGR01352; tonB Cterm; 1.
Transport; Protein transport; Transmembrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U39558; AAC44660.2; -. EMBL; AE004530; AAG04360.1; -.
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MEDLINE=20437337; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
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J. Bacteriol. 178:7059-7068(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dennis J.J., Lafontaine E.R., Sokol F "Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
                                                                                                                                                                                                                                 DROHY
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E83525; E83525.
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                                                                                                                                                                                                                                                                                                                                                                                               АҮКАЕАККҮАКААКАЕККЕҮАААЕАККАЕААКАҮКАЕААКАААКЕААҮЕА
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347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.A.
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16
37
347
216
                                                                                                                  protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                               t sequence up
t annotation of
n mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 179;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
PERIPLASMIC (POTENTIAL).
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sokol P.A.;
                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEDD4B04AA095945 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                  update)
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f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
.9e-05;
                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                   204
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MST2_DROHY
                                                                                                                                                                                                                                                                                                                                                                                                                 片
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                         "Tandemly arranged repeats of a novel highly charged 16-amino-action motif representing the major component of the sperm-tail-specific axoneme-associated protein family Dhmst101 form extended alpha-helical rods within the extremely along."
                                                                                                                                                                                                                                                                                                                         MST2_DROHY
Q08696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The Drosophila hydei gene Dhmst101(1) encodes repetitive, axoneme-associated protein with dif Y chromosomal deletion mutant flies.";

Dev. Biol. 162:414-408:770004
                                                                                                                                                                                     Bukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel.
01-FEB-1995 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN 1
ASSOCIATED WITH AXONEMAL STRUCTURES.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By 6
-!- TISSUE SPECIFICITY: TESTIS. LOCATED IN
                                                                                                                             SEQUENCE FROM N.A., AND CHARACTERIZATION MEDLINE=95045538; PubMed=7957199;
                                                                                                                                                                                                                                                  MST101(2)
                                                                                                                                                                                                                                                                                                            01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sperm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., TISSUE=Testis;
                                                                                                                                                                                                                                  Drosophila hydei (Fruit fly)
                                                                                                                                                                                                                                                               Axoneme-associated protein mst101(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0011816; Dhyd\mst101(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94200512; PubMed=8150205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in itself and this statement is not removed. Usage by and for content and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN
                FUNCTION: POSSIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPERMATID BUNDLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; X73480; CAA518
S34153; S34153
                                                                                                                                                                                                                                                                                                                                                                                                                125
                                                                                                                                                                                                                                                                                                                                                                                                                                           50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
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                              Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                AKEAAKAKKEAYKAEAKKYAKAAKAEKKEYAAAEAKK-AEAAKAYKAEAAKAAAKEAA 106
                                                                                                                                                                                                                                                                                                                                                                                                                CAEAAKKEKEA--AEKKKCAEAAKKEKE---AAEKKKCAEAAKKEKEAAEKKKCAEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKKYAKKAEK----AYAKKAKAAKEKKAYAKKEAKAYKAAE-----AKKKAKAEAKKY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        АККЕКЕАЛЕКККСАЕЛАККЕКЕЛАЕКККСАЕЛАККЕКЕЛАЕКККСАЕЛАККЕКЕЛАЕККК 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA51875.1;
                                                                                                                                                                                                                                                                                                                                         STANDARD;
               225:1089-1095(1994).
SSIBLE STRUCTURAL ROL
                                                                                                                                                                                                                                                                         31, Created)
31, Last sequence update)
40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37793 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family.
Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 X 16 AA APPROXIMATE TANDEM REPEATS K-K-K-C-X-E-X-A-[KQ]-K-X-X-E-X-A-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 175.5; DB 1
Pred. No. 3.1e-05;
                                                                                                    a novel highly charged 16-amino-acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24C65D2510387E2A CRC64;
                                                                                                                                                                                                                    Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
               ROLE
                                                                                                                                                                                                                                                                                                                                         1391 AA
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                SHI
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N SPERMATOCYTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              des a testis-specific, differential abundanc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35,
                SPERM
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RESULT 6
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Best Local S
Matches 54
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21-JUL-1986
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H1_PARAN
P02256;
                                                                                                                                                                                 Strickland W.N., Strickland M., Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                  "The primary structure of histone H1 from sperm of the sea urchin Parechinus angulosus. 1. Chemical and enzymatic fragmentation of t protein and the sequence of amino acids in the four N-terminal cyanogen bromide peptides.",

Eur. J. Biochem. 104:559-566(1980).
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-84.
MEDLINE-80156831; PubMed-6767609;
Strickland M.N., Strickland M., de
Wittmann-Liebold B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parechinus
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0020733; Dhyd\mst101(2).

Sperm; Repeat; Multigene family; Polymorphism.

Sperm; Repeat; Multigene family; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X73481; CAA51876.1; -. PIR; S51364; S51364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the entire primary structure.";
Eur. J. Biochem. 104:567-578(1980)
                                                                                                                                       "The primary structure of histone Parechinus angulosus. 2. Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Histone H1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                            SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Echinoidea; Euechinoidea;
                                                                                                                                                                                                                     MEDLINE=80156832; PubMed=7363905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN Buropean Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPERMATIDS.

DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL.
POLYMORPHISM: LENGTH POLYMORPHISMS EXIST BETWEEN DI
STRAINS, MOST LIKELY CAUSED BY LENGTH VARIATIONS WI
                SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: SP
                                                         . J. Biochem. 104:567-578(1980).
FUNCTION: HISTONES H1 ARE NECESSARY
NUCLEOSOME CHAINS INTO HIGHER ORDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1068
  SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEEAAKREKEA--AEKKKCAEAAKKEKE--ATEKQKCAEAAKKEKEAABKKKCAEAA 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      АКЕЛАКАККЕЛУКЛЕЛККУАКЛАКАЕККЕУАЛАЕЛККАЕЛАКАУКЛЕЛАКАЛАКЕЛА 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKKLKEAAEKKQCEERAKKEKEAAEKKQCEERAKKLKEAAEKKQCEERAKKEKEAAEKKR 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AKKYAKKAEKAY----AKKAKAAKEKKAYAKKEAKAYKAAE-----AKKKAKAEAKKY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               angulosus (Angulate sea urchin).
Metazoà; Echinodermata; Eleutherozoa;
; Euechinoidea; Echinacea; Echinoida; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1391 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 01, Created)
(Rel. 01, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                              80-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gonadal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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46.2%;
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SPERM.
TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TESTIS. PRIMARY SPERMATOCYTES
                                          Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 171.5; DB Pred. No. 0.00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             de
                                                                                                                                                                                                    Brandt W.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1B2A368F30F48878 CRC64;
                                                                                                                                         c H
                                                                                                                                                                                                                                                                                                                                                                                                          Groot P.C.,
                                                                                                                                           from
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(See http://www.isb-sib.ch/announce/
                                                           FOR THE CONDENSATION STRUCTURES.
                                                                                                                                         m sperm of t
C-terminal
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                                                                                                                                                                                                      Yon
                                                                                                                                                                                                                                                                                                                                                                                                          von Holt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Echinidae;
                                                                                                                                                                                                    Holt C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                            sea urchin
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                                                                                                                                         peptide
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Best Local (
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InterPro; IPR005819; Histone H5.
InterPro; IPR005216; Linkerhist N.
Pfam; PF00538; linker histone; T.
PRINTS; PR00624; HISTONEH5.
PRODOm; PD000373; Linkerhist_N; 1.
SMART; SM00526; H15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sperm.
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H1B_STRPU STANDARD; PI
P15869;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seque
15-JUL-1999 (Rel. 38, Last annot
Histone H1-beta, late embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                InterPro; IPR005818; Histone_H1/H5
InterPro; IPR005819; Histone_H5.
InterPro; IPR005216; Linkerh1st N.
Pfam; PF00538; linker histone; I.
PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strongylocentrotus purpuratus.";
Mol. Cell. Biol. 8:1842-1844(1988).
-i- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lai Z.-C., Childs G., "Characterization of the structure the gene encoding the late histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=88246461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus.
NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                     SMART; SM00526; H15;
                                                                                                                                                                                                                                   PIR; A28100; A28100.
HSSP; P02259; 1HST.
                                                                                                                                                                                                                                                                                   EMBL; M20314; AAA30052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chromosomal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A91090; HSUR1P.
HSSP; P02259; 1HST.
                                                                             ProDom; PD000373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES. SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKAKKTSAAAKAKAAAAAKKARKAKAAAKRKAALAKKKAAAAKRKAAAKAKKAKKPKK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 AA;
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                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                             Linkerhist_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=2837660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.9%;
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  Nuclear protein;
22169 MW; 9F21458
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Pred. No. 5e-05;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ×
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     9F214581334BBE7A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and transcriptional patterns of subtype H1-beta of the sea urch
        DNA-binding; Multigene
81334BBE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₹
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                                                                                                                                                                                                                                                                                                                                                                    http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration -
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RESULT FACTOR OF THE TOTAL TOT
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RA Adams D., Function Y. J., R., Evans C.A., Gocayne J.D., Andanatides P.G., Scherer S.E., Hilp P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Burton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ra Ballew R.M., Bauck J., Brokstein P., Brottier P., Ra Borkova D., Benche P.V., Berman B.P., Bhandari D., Bolahakov S.M., S., Challew R., Carley S., Dahike C., Davenport L.B., Davies P., Ra Borkova D., Benche P.V., Berman B.P., Carley R., Charde R., Chardra I., Charley R., Charden R., Dew I., Dietz S.M., Podeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Polec C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wein M.-H., Ibegwam C., Laiko P., Lei Y., Hernander J., Wein M.-H., Ibegwam C., Laiko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M., Ra Ra Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M., Ra Ra Melson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H., Ra Nice B.C., Stden-Kiamos I., Sampson M., Stupski M.P., Smith T., Shen H., Santh T., Shen H., Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Wilsias R., Tector C., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Beoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9VGX3; Q95S18; Q9VGX1; Q9VGX2; Q9Y0F9;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence upd
15-SEP-2003 (Rel. 42, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAU
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STRAIN=Canton-S; TISSUE=Head;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ma E., Xu T., Haddad G.G.; "Gene regulation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99097004; PubMed=9878744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phila melanogaster.";
Res. Mol. Brain Res.
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llarity 48.7%;
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Pred. No. 5.1e
8; Mismatches
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Alternative splicing.
DOMAIN 88 143
DOMAIN 354 668
VARSPLIC 26 131

ALA/GLU-RICH.

YPSVEKVTRYYKSYPIYSSYSVPRRVYGATRVVTSPIRVV
TSPARVVSRUHSPSPVRVVRTTTRVISSPERTTYSYTTPS
TYYSPSYLPSTYTSTYIPTSYTTY -> TPRLDLCTDRPGS
HRSRASSDYSYTSKSSVEKSSYDSSNPHSYRPERSTYTSTV
EKTSRSGPGGSYNYSTERTSTTGAGPGGYSYSSTTSGNLPG

GO; GO:0006979; P:response

6

stress;

THR-RICH oxidative

FlyBase;

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EMBL; AP154418; AAD38397.1; --
EMBL; AB003688; AAF54550.1; --
EMBL; AE003688; AAF54550.1; --
EMBL; AE003688; AAF54551.1; --
EMBL; AB003688; AAF54552.1; --
EMBL; AY0060997; AAL28545.1; --
EMBL; AY119569; AAM50223.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ye J., Yeh R
Zheng X.H.,
Gibbs R.A.,
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Lewis S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The
                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu
Stapleton M., Carlson J.W., Brokstein P., Yu
George R.A., Guarin H., Kronmiller B., Pacleb
Rubin G.M., Celniker S.E.;
"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(
-!- FUNCTION: Plays an important role in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Dryddale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Annotation of the Drosophila melanogaster euchromatic
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                                                                                                                                                                                                                                                                                                                                                                                      i- INDUCTION: By anoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9VGX3-5; St
TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (, Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., 19 X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., 18 R.A., Myers E.W., Rubin G.M., Venter J.C., 19 genome sequence of Drosophila melanogaster.", nce 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q9VGX3-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9VGX3-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comment=Experimental
                                                                                                                                                                                                                                                                                                                                                                                                      neurons and cortical neurons of central brain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Head
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence=VSP_004052;
Y: Concentrated in la
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, Pacleb J.M.,
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Best Local S
Matches 55
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15-JUL-1999 (Rel. 38, Last annotation update)
Histone H1.10 (Methylated DNA binding protein-2-H1) (MDBP-2-H1).
Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasian
          Schwarz S., Hess D., Jost J.P.;
"The methylated DNA binding protein-2-H1 (MDBP-2-H1) consists into methylated by hich are truncated at the C-terminus."; Nucleic Acids Res. 25:5052-5056(1997).
-I- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION ONUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
                                                                                                                        SEQUENCE FROM N.A.

MEDLINB=87250632; PubMed=3597432;

MEDLINB=87250632; PubMed=3597432;

Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;

Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;

Characterization of the chicken histone H1 gene complement.

Generation of a complete set of vertebrate H1 protein sequent.

J. Biol. Chem. 262:9656-9663(1987).
                                                                                                                                                                                                                                                                                          01-AUG-1988 (Rel.
01-NOV-1997 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                     P08286;
01-AUG-1988
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                                                                       IDENTIFICATION OF ALA-13.
MEDLINE=98060905; PubMed=9396815;
Schwarz S., Hees D., Jost J.P.;
SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                 _TaxID=9031;
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41.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKSSYPIVSSYSVPRRVYGATRVVTSPIRVVTSPARVVSRV
IHSPSPVRVVRTTTRVISSPER -> SIWFSSLSPTSLVII
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PYVSTRDKNRTRILGMVRQHIDTVEAGGNTAGRTFRDSLDA
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RSSLSPLRITPSPVR -> RTKRTPIDWEKVPFVPRPSLIS
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/FTId=VSP_004047
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RESULT 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                        Yelton D.B., Limberger R.J., Curci K., Malinosky-Rummell Sliviensky L., Schouls L.M., van Embden J.D., Charon N.W. "Treponema phagedenis encodes and expresses homologs of tpallidum TmpA and TmpB proteins.";
Infect. Immun. 59:3685-3693(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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EMBL; M58563; AAA27480.1; PIR; B43592; B43592.
                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                       Treponema phagedenis.
Bacteria; Spirochaetes;
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                         NCBI_TaxID=162;
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    -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.

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Pro; IPR005819; Histone_H5.
PF00538; linker_histone; 1.
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Last annotation updat
Protein B precursor (An
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Pred. No.
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RESULT 11
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Matches 52
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P08287;
01-AUG-1988
01-AUG-1988
28-FEB-2003
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REPEAT
                                                                                                                                SEQUENCE FROM N.A.

MEDILINE=87250632; PubMed=3597432;

Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;

Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;

"Characterization of the chicken histone H1 gene compl
Generation of a complete set of vertebrate H1 protein
J. Biol. Chem. 262:9656-9663(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                      CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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MEDLINE=94032251; PubMed=8218199; Cerf C., Lippens G., Muyldermans S., Segers A., Ramakrishnan V., Wodak S.J., Hallenga K., Wyns L.; Segers A., Ramakrishnan V., Wodak S.J., Ramakrishnan V., Segers A., Ramakrishnan V., Ramakrish
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken)
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21 POTENTIAL.
2384 TREPONEMAL MEMBRANE PROTEIN B.
2384 TREPONEMAL MEMBRANE PROTEIN B.
27 X 5 AA TANDEM REPEATS OF K-A-A-[AKR]-
28 [ED].
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6 X 8
2-A-B-B
2-2.
2-3.
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                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                   Phasianidae; Phasianinae;
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                                                                                                                                                                    complement.
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RESULT 12
H1_ONCMY
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P06350;
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INIT_MET
MOD_RES
                                                                                                                                                                                        Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; B. Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncori NCBI_TaxID=8022;
                                                    Mezquita J., Connor W., Winkfein R.J., I
"An H1 histone gene from rainbow trout (
J. Mol. Evol. 21:209-219(1985).
-I- FUNCTION: HISTONES H1 ARE NECESSARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 32:11345-11351(1993).

1- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.

1- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                       01-JAN-1988
15-JUL-1999
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                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=85264847; PubMed=6443128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR005818; Histone_H1/H5
InterPro; IPR005819; Histone_H5.
Pfam; PP00538; linker_histone; 1.
NUCLEOSOME CHAINS INTO HIGHER ORDER SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE HISTONE !
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49; Conserv
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(Rel.
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43.8%;
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Pred. No. 0.000
13; Mismatches
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  HISTONE H1/H5 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                       206
                                                                                                                                                                                                                                                                                                                       update)
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                                                                                                                       Dixon
                                                                                                  (Salmo
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                                                                                                                       G.H.;
                                                                                                gairdnerii).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 224;
                                                              CONDENSATION
                                                                                                                                                                                                                       Oncorhynchus.
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RESULT 13
H15_HUMAN
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Best Local S
Matches 52
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P16401; Q14529;
01-AUG-1990 (Rel. 15, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Histone H1.5 (Histone H1a).
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SMART; SM00526; H15; 1.
Chromosomal protein; Nuclear
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SEQUENCE FROM N.A.

MEDLINE=22296985; PubMed=12408966;

Marzluff W.F., Gongidi P., Woods K.R., Jin

"The human and mouse replication-dependent
Genomics 80:487-498(2002).
                                                                                                                                                                                                                             Ohe Y., Hayashi H., Iwai K.;
"Human spleen histone HI. Isolation
minor variants, HIa, HIc, and HId.";
J. Biochem. 106:844-857(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=97183654; PubMed=9031620;
Albig W., Meergans T., Doenecke D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005818; Histone_H1/H5.
InterPro; IPR005819; Histone_H5.
Pfam; P700538; linker histone; 1.
PRINTS; PR00624; HISTONEH5.
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                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                MEDLINE=90130391; PubMed=2613692;
                                                                                                                                                                                                                                                                                                                    (ISSUE=Spleen
                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acetylation.
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                                                                                                                                         Characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A02584; HSTR1R.
                                                                                                         184:141-148(1997).
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                                                                                                                       genes.";
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27
206 AA;
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· 20672 MW;
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Primates;
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                                                                                                                                        Doenecke
he H1.5 ge
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                         gene
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                                                                                                                                                                                                                                                               amino acid sequences
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                  J., Malt
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RESULT 14
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Best Local Similarity
Matches 51; Conserv
smegmatis.";
Mol. Gen. Ge
-i- FUNCTION
                                                                                                                                                                                                                                                                                                                                         Q9ZHC5;
16-OCT-2001
16-OCT-2001
16-OCT-2001
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INIT_MET
MOD_RES
CONFLICT 2
                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 700084 / mc(2)155;
MEDLINE=99110209; PubMed=9894918;
Lee B.H., Murugasu-Oei B., Dick T
"Upregulation of a histone-like p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HISTONES HI ARE NECESSARY FOR THE CONDENSATION
NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
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SMART; SM00526; H15; 1.
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GO; GO:0003677; F:DNA binding activity; NAS.
GO; GO:00007001; P:chromosome organization and
GO; GO:0006334; P:nucleosome assembly; NAS.
InterPro; IPR005818; Histone H1/H5.
InterPro; IPR005819; Histone H5.
Pfam; PF00538; linker histone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S51660; S51660.
HSSP; P08287; 1GHC.
Genew; HGNC:4719; HIST1H1B
                                                                                                                                                                                                NCBI_TaxID=1772;
                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae;
Corynebacterineae; Mycobacteriaceae; Mycobac
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SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
    FUNCTION:
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225 AA;
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Pred. No. 0.000
7; Mismatches
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MISSING (IN REF. 1).
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                                                                    c T.;
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MBL outstation -
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RESULT 15
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Best Local
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01-AUG-1988
15-SEP-2003
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the Euro
                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sisb-sib.ch).
                                                                                                                                                                                                                   MEDLINE=87250632; PubMed=3597432;
Coles L.S., Robins A.J., Madley L.K., Wells J.R.E.;
"Characterization of the chicken histone H1 gene complement.
Generation of a complete set of vertebrate H1 protein sequences.
J. Biol. Chem. 262:9656-9663(1987).
J. FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF NUCLESCOME CHAINS INTO HIGHER ORDER STRUCTURES.

-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMAKI; SHOUTAL, J...., PROSITE; PROSONAS, HISTONE LIKE; 1.

DNA-binding; DNA condensation; Repeat.

DOMAIN 1 90 BACTERIAL HISTONE-LIKE DOMAIN.

DOMAIN 101 205 DEGENERATE REPEATS REGION.

DOMAIN 101 205 DEGENERATE REPEATS REGION.

CECUTENCE 208 AA; 21230 MW; CASF577F61F7EF09 CRC64;
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Pfam; PF00216; Bac DNA binding; 1.
ProDom; PD000945; Bac DNAbind; 1.
SMART; SM00411; BHL; I.
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             EMBL; M17020;
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                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
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Best Local Similarity
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InterPro; IPR005819; Histone H5.
Pfam; PP00538; linker histone; 1.
PRINTS; PR00624; HISTONEH5.
SMART; SM00526; H15; 1.
                                                                                                                                                     INIT MET
                                                                                                                                        SEQUENCE
                                                                                                                                                                          3D-structure.
                                                                                                                                                                                      Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
                                                                                                                                                                                                                                                          PDB; 1GHC; 31-AUG-94.
                                              109
 169
                       58
                                                                                           52;
                                                                1 AKKYAKKAEKAYAKKAKAAKEKKAYAKK---EAKAYKAABAKKKAKAEAKKYAKEAAKAK 57
                 KEAYKAEAK-KYAKAAKAEKKEYAA-AEAKKAEAAKAYKAEAAKAAAKE 104
SKKPGEGLEKAPKKKASAAKPKKAAAKKPAAAAKKPKKAVAVKKSPKKAKKPAASATKKS
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                                                                                            Conservative
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                                                                                                                                        CB9724BFF14654A6 CRC64;
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1: sp_acteria:*

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5: sp_invertebrate

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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01-JUN-2002
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01-NOV-1999
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Plasmodium vivax.
Eukaryota; Alveolata;
NCBI_TaxID=5855;
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InterPro; IPR006260; TonB C.
PRINTS; PR00624; HISTONEH5.
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Rodriguez-Herva J.J., Ramos Gonzalez M.I., Ramos J.;
"The Pseudomonas putida peptidoglycan-associated outer membrane lipoprotein (PAL) is involved in maintenance of the integrity o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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Submitted (JUL-1999)
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372 AA; 40133 MW; 87F4
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4; Mismatches 31
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SEQUENCE FROM N.A.
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STRAIN=Salvador;
STRAIN=Salvador;
Michon P., Stevens J.R., Kaneko O., Adams J.H.;
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Q8ZQT6
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MEDLINE=22388234; PubMede112471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch

Rasko D., Buckles E. L., Liou S.-R., Boutin A., Hackett J., (

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome
of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli O6.
Bacteria; Proteobacteria;
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421 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKKAEKAYAKKAKAAKE----KKAYAKKEAKAYKAAEAKKKA-----KAEAKKYA
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                                                                                                                                                                                                                                                                                                               АККЕАУ-КАЕАККУАКААКАЕККЕУААЛЕАКК---АЕЛАКАУКАЕЛАКАААКЕАА
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Pred. No. 2.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 188.5; DB 1
Pred. No. 9.6e-06;
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MEDLINE-21156231; PubMed-11258796;

MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genome sequence of enterohemorrhagic Train K-12.";
                                                                                                                                                                                                                                                                                                                                                                  Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kitkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck B.J., Davis N.W., Lim A., Dimalanta B.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
Nature 409:529-533 (2001).
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MEDLINE=21534948; PubMed=11677609;

McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreill Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Lay Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney Depart S., Weyner C., Scott K., Holmes A., Grewal N., Mulvaney
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Bacteria; Proteobacteria;
Enterobacteriaceae; Salmor
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MEDLINE=21074935; PubMed=11206551;
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Enterobacteriaceae; Escherichia.
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Escherichia coli O157:H7.
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01-OCT-2002 (TrEMBLrel.
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01-MAR-2002
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EMBL; AE008730; AAL19691.
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    20, Last sequence update)
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spanning protein.

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Pred. No. 1.
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                                                                                                                                                    K., Yokoyama K.,
M., Tobe T.,
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RESULT 8
Q8ZGZ2
ID Q8ZG
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Q8ZGZ2 Q8ZGZ2; 01-MAR-2002 01-MAR-2002 01-MAR-2003

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Matches 58
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Best Local
                                                                                                                                                                                                                                                                                                       Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21534947; PubMed-11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain in Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Baker S., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamilin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 8:11-22(2001).
EMBL; AB005252; AAG55075.1; -.
EMBL; AP002553; BAB34197.1; -.
InterPro; IPR000104; Antifreeze_1.
PRINTS; PR00308; ANTIFREEZEI.
Complete proteome.
Complete 394 AA; 40517 MW; 5B58D8E8230BDE28 CRC64;
                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of a multiple drug resistant Salmonella enterica server Typhi (T18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CT18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi
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191
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376 AA;
                                                                                                                                   AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA
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-KAEAEAAKAAADAKKKADAEAAKAAAEAKKKADAAAAKAAADAKKKAAAE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEEAAKQAELKQKQAEEAAAKAAADAKAKAEADDKA--AEEAAKKAAADAKKKAEAEAAK
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                                              ҮКАЕАККҮАКААКАЕККЕҮАААЕАККАЕААКАҮКАЕААКААА---КЕААҮЕ 108
                                                                                                  AKAAADAKKKAEAEAAKAAADAKKKAEAEA-AKAAADAKKKAEAEA---AKAAAEAKK--
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                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                             38804 MW;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                     Score 178; DB 16;
Pred. No. 4.5e-05;
0; Mismatches 33
                                                                                                                                                                                                                                                                                                               EC21F2C4767A8A42
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                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                      Length
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RESULT
Q8CZZ8
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Best Local S
Matches 63
                                                   Query Match
Best Local S
Matches 63
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                                                                                                                                                                                               SEQUENCE FROM N.A.
STRALN=KIM5 / Biovar Mediaevalis;
STRALN=KIM5 / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mensey W., Burland V., Plankett G. III, Boutin A., Merry Parketterston J.D., Lindler L.E., Brubaker R.R., Planketterston J.D., Lindler L.E., Brubaker R.R., Planketterston J.D., McDonough K.A., Milles M.L., Matson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8CZZ8;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                       Membrane spanning TOLA OR Y3056.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8CZZ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome. SEQUENCE 388 AA;
                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     Yersinia pestis.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CO-92 / Biovar Orientalis;
MEDLINE=21470413; PubMed=11586360;
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TOLA OR YPO1123
                                                                                                                                         EMBL;
                                                                                                                                                    "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
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Vature 413:523-527(2001).
SMBL; AJ414146; CAC89966.1; -.
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                                                                                                                                      AE013906; AAM86606.1;
                                                                                                                                                                                        R.D.;
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                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                     41012 MW;
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                                                                    34.3%;
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                                                       12;
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2; Mismatches
                                                                                    Score 178;
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                                                                                                                       1E3E4FF87E533481 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393
                                                   4.7e-05;
ches 28;
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                                                                                      DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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                                                                                                                                                                                                      Plano G.V.
                                                                                                                                                                                                                                                                                                                                                                      Enterobacteriales;
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                                                                                      Length
                                                                                                                                                                                                                                                      Mayhew G.F.,
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                                                       Indels
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                                                                                       393;
                                                                                                                                                                                                         Blattner
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                                                       Gaps
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SOR READ AND COCCUPANT OF THE PROPERTY OF THE

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RESULT 11
Q9CM70
ID Q9CM7
AC Q9CM7
AC Q9CM7
DT 01-JU
DT 01-JU
DT 01-OC
DE TolA.
GN TOLA.
GN TOLA
OS Paste
OC Paste
OC Paste
OC Paste
OC NCB1
RN [1]
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Q8XVN7
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Best Local S
Matches 67
                                                                                  Q9CM70;
Q9CM70;
01-JUN-2001
01-JUN-2001
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8XVN7
Q8XVN7;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                         Salanoubat M., Génin S., Artiguenave F., Gouzy J., Mangeno Arlat M., Billault A., Brottier P., Camus J.C., Cattolico Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Dem Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schi Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacea: Nature 415:497-502(2002).
                      Pasteurella multocida.
Bacteria; Proteobacteria; Gan
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ralstonia solanacearum (Pseudomonas Bacteria; Proteobacteria; Betaprotec Ralstoniaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome
SEQUENCE 200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-GMI1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probable histone H1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR005819; Histone_H5.
PRINTS; PR00624; HISTONEH5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSC2793 OR RS00453.
                                                             TOLA OR PM0968
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                                                                                                                                                                                                                                                                                                                                            l Similarity
67; Conserv
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                                                                                                                                                                                                                        YEA 109
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                                                                                                                                                                                                                                                 АКАККЕЛУКАЕЛККУАКАЛК-----ЛЕККЕУЛЛЕЛККАЕЛАК---ЛУКЛЕЛАКАЛАКЕЛ
                                                                                                                                                                                                                                                                                                AKKVA--AKKVAAKKAPAAKKAAVKKVAAKKAAPAKKAAVKKVAAKKAPAAKKAAVKKVA
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                                                                                                                                                                                                                                                                                                                                                                                               200 AA;
                                                                                    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               19279 MW;
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                                                                                     17,
17,
22,
                                      Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                              Score 176.5; I
Pred. No. 3.2e
5; Mismatches
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Last annotation update)
                                                                                     Last annotation
                                                                                                            Created)
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                                                                                                sequence update)
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                                       Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                 Indels
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Q39576
ID Q3957
AC Q3957
AC Q3957
AC Q3957
O1-WC
DT 01-WL
DT 01-WL
DT 01-WL
CGN CH1an
OC Eukar
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DT OS116
DT OS1-AL
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Best Local S
Matches 54
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Best Local (
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Kappe S.H.I., Noe A...,
"A family of chimeric erythrocyu-
"A family of chimeric erythrocyu-
"Barasites.";
parasites.";
par
                                                                                                                    01-NOV-1996
01-NOV-1996
01-MAR-2003
                                                             Histone
CH1.
                                                                                                                                                                                                           Q39576;
Q39576;
   Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae;
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Eukaryota; Alveolata; Api
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01-OCT-2002
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01-AUG-1998
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MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam
"Complete genomic sequence of Pasteurella multocida
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
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                                                                                                                    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.9%; Score 170.5; 53.5%; Pred. No. 0.0
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48.7%; Pred. No. 9.4
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                                                                                                                    23,
Chlorophyta;
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Last annotation update)
                                                                                                                 Last sequence update)
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Chlorophyceae; Volvocales;
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Best Local
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O01395;

O1-JUL-1997 (TrEMBLrel. 04, Created)

O1-JUL-1997 (TrEMBLrel. 04, Last sequen.

O1-CCT-2002 (TrEMBLrel. 22, Last annota.

Axoneme-associated protein MST101(3).

MST101(3) OR DHWST101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0624; HISTONEHS.
ProDom; PD000373; Linkerhist N; 1.
SMART; SM00526; H15; 1.
SEQUENCE 232 AA; 24693 MW; 2D0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The organization structure and regulatory elements of Chlamydon histone genes reveal features linking plant and animal genes.", Curr. Genet. 28:33-345(1995).
EMBL; U16726; AAA98452.1; -.
HISSP; P02259; 1HST.
                                                                                                                                                                                                      Neesen J., Heinlein U.A.O., Buenemann H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE SPERM TAIL
                                                                                                                                                                                                                                                                                    Drosophila hydei (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR005818; Histone H1/H5
InterPro; IPR005819; Histone H5.
InterPro; IPR003216; Linkerhist N.
Pfam; PF00538; linker histone; I.
                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3055;
                                                                                                                                    -!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL EMBL; U85627; AAB51369.1; -.
                                                                                                                                                               -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96120862; PubMed=8590479; Fabry S., Muller K., Lindauer A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                         FlyBase;
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                                                                                                                                                                                          SIMILARITY)
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                                                                    se; FBgn0020732; Dhyd\mst101(3).

Repeat; Multigene family.

13 x 16 AA APPROXIMATE TANDEM REPEATS

64 255 13 x 16 AA APPROXIMATE TANDEM REPEATS

X-[KQ]-K-C-[AB]-E-X-A-[X]-K-X-X-X-X-

[AB]-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 ----AKAKKEAYKAEAKKYAKAAKAEKKEYAAAE----AKKAEAAK----AYKAEAAKAAAK 103
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                                                      275 AA;
 Conservative
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Pred. No. 0.0001;
0; Mismatches
Score 169.5; DB 5
Pred. No. 0.00013;
6; Mismatches 29
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                                                       76BAA7B2A2DF732C CRC64;
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annotation update)
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Chlamydomonas
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RESULT 15
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Search completed: January 21, 2004, 09:00:27 Job time: 44.8831 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92119224; PubMed=1731966;
Wakarchuk W.W., Muller F.W., Beck C.F.;
Wakarchuk W.W., Muller F.W., Beck C.F.;
"Two GC-rich DNA elements of Chlamydomonas reinhardtii with complex arrangements of directly repeated sequence motifs.";
Plant Mol. Biol. 18:143-146(1992).
EMBL; X17208; CAA35080.1; -.
NON TER
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SEQUENCE 265 AA; 26216 MW; B35318B7377CF782 CRC64;
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
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Q39598; O1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
CGCT-4 product (Fragment)
CGCR-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyright
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /geneseq/geneseqp-emb1/AA1980.DAT:*
/geneseq/geneseqp-emb1/AA1981.DAT:*
/geneseq/geneseqp-emb1/AA1982.DAT:*
/geneseq/geneseqp-emb1/AA1983.DAT:*
/geneseq/geneseqp-emb1/AA1984.DAT:*
/geneseq/geneseqp-emb1/AA1985.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
No.	Score	Match	Match Length DB	ВВ	Ħ	Description
ב	519	100.0	109	21	AAY82577	Copolymer molecula
2	312.5	60.2	96	21	AAY82576	Copolymer molecula
ω	289	55.7	77	21	AAY82575	Copolymer molecula
4	228.5	44.0	66	21	AAY82574	Copolymer molecula
ហ	209	40.3	154	Ľ	AAR06445	Recombinant copoly
თ	187	36.0	106	ļ	AAR06446	Recombinant copoly
7	180.5	34.8	56	21	AAY82573	Copolymer molecula
8	179.5	34.6	100	21	AAY98499	Peptide #10 used i
9	179.5	34.6	100	21	AAY59044	Amino acid polymer

ALIGNMENTS

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RESULT 1
AAY8257
ID AAY8
AXY AAY8
AC AAY8
AC AAY8
AC AAY8
AC AAY8
AC Copc
XX
XX
XX
XX
COpc
XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psori Hashimoto's disease; idiopathic myxoedema; myasthenia gravis; pemphigus vulgaris; systemic lupus erythematosus.
                                                                                                    25-SEP-1998;
                                                                                                                                                                                                             24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
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(YEDA ) YEDA RES & DEV CO LTD
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                                                                                                         98US-0101693.
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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, or system lupus erythematosus. Mediated-mediated diseases which can be treated include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
                Unidentified
                                                     pemphigus vulgaris;
                                                                           Hashimoto's disease; idiopathic myxoedema; myasthenia
                                                                                            Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis;
                                                                                                                                 antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis;
                                                                                                                                                                    glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective; osteopathic; immunosuppressive; antihyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
                                                                                                                                                                                                                                   Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                          Copolymer molecular weight TV-marker amino acid sequence SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                           AAY82576 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 14; 72pp; English
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ilarity 100.0%;
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                                                         lupus
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Pred. No. 1.5
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                                                       erythematosus
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s 0;
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RESULT 3
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ID AAY8
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AC AAY8
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Best Local
                 Copolymer; molecular weight marker; TV-marker; immune disease; glatiramer acetate; autoimmune disease; antiarthritic; neuroprostepathic; immunosuppressive; antithyroid; antiinflammatory;
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                                                                                                                                                                                                             AAY82575 standard; peptide;
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                                                                                           Copolymer molecular weight TV-marker amino acid sequence
                                                                                                                                   28-JUL-2000
                                                                                                                                                                        AAY82575;
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(TEVA-) TEVA PHARM USA
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Pred. No. 2.2e-19;
1; Mismatches 3
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antidiabetic; thyromimetic;

haemostatic;

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RESULT 4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antianaemic; immunosuppre inflammatory condition; m Crohn's disease; chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be used for treating and preventing immune diseases in a mammal. Autoimmune diseases which may be treated include either cell-mediated or antibody-mediated diseases. Such diseases include arthritic conditions, demyelinating diseases and inflammatory conditions, e.g. multiple
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(TEVA-)
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                               AAY82574 standard; peptide; 66 AA
                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                        weight markers.
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PHARM USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which has an identified molecular weight
                                                                                                                                                                                                                                                                1:
                                                                                                                                                                                                                                                                Score 289; DB 21;
Pred. No. 1.8e-17;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecular weight markers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prevention
                                                                                                                                                                                                                                                                                                 Length 77;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of immune diseases
                                                                                                                                                                                                                                                                  32;
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AAY82574

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АККУАККАЕКАУАККАКААКЕККАУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕА 60

· EAKAAKKA - - - ·

25

YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAAKEAAYEA

Matches Query Match Best Local

62;

Conservative

0;

Mismatches

Indels Length

43;

Gaps

Similarity

44.0%;

Score 228.5; DB Pred. No. 1.8e-12

21;

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weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight of a copolymer (CP), which has an identified molecular weight cand an amino acid composition corresponding to the copolymer. The polypeptides of the invention are used as molecular weight markers for glatiramer acetate related tetrapolymers. The polypeptides may also be composed to the copolymer. The colypeptides may also be composed to the copolymer. The polypeptides may also be considered the copolymer of the copolymer. The polypeptides may also be considered the copolymer of the copolymer. The polypeptides may also be considered the copolymer of the copolymer of the copolymer. The polypeptides may also be considered the copolymer of the copolymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copolymer; molecular weight marker; TV-marker; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glatiramer acetate; autoimmune disease; antiarthriti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copolymer molecular weight TV-marker amino
                                                                            include host-versus-graft disease, graft-versus-host disease, and delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gad A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY82571 to AAY82577 represent specifically claimed copolymer molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-317499/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pemphigus vulgaris; systemic
                                                   molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TEVA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (YEDA )
                                                                          atiramer acetate molecules,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEDA
66
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A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US22402
                                                      markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEV CO LTD
USA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lupus erythematosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lc; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases
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RESULT 5

AAR06445 standard;

protein;

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                                                            Matches
                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                    To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-77 were subcloned from pERV 2.1 to pBG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-19910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-77 contains oligonucleotide duplexes incoding the following segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alanine residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-1990;
17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant copolymer 1; COP-1-77; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
03-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR06445;
                                                                                                                                                                                                      segments: YKK, EAE, KAK, AAK, and AAA. The N-terminal alanine re is left behind following CNBr cleavage of the fusion protein. The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or control edemyelinating disorder, e.g. multiple sclerosis. They may also be used as additives to hair care products to confer beneficial be used as additives to hair care products to confer beneficial effects on damaged hair or as supplements for diets deficient in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing genes encoding random polymers of aminoacid(s) - producing recombinant polypeptide(s) with biological and/or immunological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant
                                                                                                                                                                         certain amino acids.
See also AAQ05665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 11; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REPK ) REPLIGEN CORP.
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24
                            N
                                                            Similarity 72; Conserv
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 KKKAKBABKAKKAKYKKYKXEABAAKAAKAAAAAAYKKBABA--AABAEKAKYKKKAKBA
                              KKYAKKAEKA-----YAKKAKAAKEKKAYA----KKEAKAYKAAEA-----KKKAK-A 44
                                                                                                                            154
                                                          40.3%; ilarity 53.7%; Conservative
                                                                                                                                                          25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copolymer 1-77, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-0473845.
89US-0312541.
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                                                                                                                                                          correct
                                                            8
                                                          Score 209; DB 11;
Pred. No. 1.9e-10;
8; Mismatches 20
                                                                                                                                                          PA field.)
                                                                                          DB 11;
                                                                                          Length 154;
                                                            Indels
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                                                              34;
                                                              Gaps
 81
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Query Match Best Local Similarity

36.0%; 55.0%;

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RESULT 6
AAR06446
ID AAR0
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                                                              demyelinating disorder, e.g. multiple sclerosis. They be used as additives to hair care products to confer effects on damaged hair or as supplements for diets de see also AAQ05664.
(Updated on 25-MAR-2007
                                                                                                                                                                                                       To improve the expression of rCOP-1 polypeptides in E. coli, genes coding for rCOP-1-19 were subcloned from pRFV 2.1 to pEG3-2deltaN (deposit: 20-NOV-1984 US4691009, NRRL B-15910), a plasmid used to express Protein A. The resulting plasmids encode fusion proteins consisting of beta-glucuronidase, Protein A, and rCOP-1 sequences. A methionine residue occurs between the Protein A and rCOP-1 sequences, originating from the 5' linker sequence, in order that the COP-1 polypeptide may be cleaved from the fusion protein. rCOP-1-19 contains oligonucleotide duplexes incoding the following segments: VKX, ABA, KAX, KEA, KKA, YEA, AKA KEA, ANA KEA, and AAA. The N-terminal alanine residue is left behind following CNBr cleavage of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-1990;
17-FEB-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant copolymer 1; COP-1-19; myelin basic protein; MBP; immunological activity; autoimmune encephalomyelitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
03-JAN-1991
                                                                                                                                                             fusion protein.

The product prevents or arrests experimental autoimmune encephalomyelitis. They are used to prevent, arrest or
                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 12; 25pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                   producing genes encoding random polymers of aminoacid(s) -
producing recombinant polypeptide(s) with biological and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ06446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-255848/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cook KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant copolymer 1-19, myelin basic protein analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR06446;
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                                                                                                                                                                                                                                                                                                                                                                                                                        1mmunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REPK ) REPLIGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYKKKAKAAAEAEYKKEAEEAEYKKYKKKAKKAKYKKKAKEAEKAKAAAEAEKAKEAEYK 141
                                             106
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(first entry)
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89US-0312541.
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                                                                                                                                                                                                                                                                                                                                                                                           English.
Score 187; DB 11; Pred. No. 8.7e-09;
                                                                                                                      diets deficient in
               Length 106;
                                                                                                                                   They may also nfer beneficial
                                                                                                                                                                얶
                                                                                                                                                                  control
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RESULT 7
AAV88251
ID AAX8
XX AAX8
XX AAX8
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XX COP

                                                                                       CC Weight TV-marker polypeptides from the present invention. The present CC weight TV-marker polypeptides (I) for determining the molecular CC invention describes polypeptides (I) for determining the molecular CC invention acid composition corresponding to the copolymer. The CC weight of a copolymer (CP), which has an identified molecular weight CC and an amino acid composition corresponding to the copolymer. The CC polypeptides of the invention are used as molecular weight markers for CC glatiramer acetate related tetrapolymers. The polypeptides may also be CC used for treating and preventing immune diseases in a mammal. Autoimmune CC diseases which may be treated include either cell-mediated or CC dateases which may be treated include either cell-mediated or CC antibody-mediated diseases. Such diseases include arthritic conditions, e.g. multiple CC sclerosis, rheumatoid arthritis, osteoarthritis, autoimmune haemolytic canaemia, autoimmune cophoritis, autoimmune thyroiditis, autoimmune CC uveoretinitis, Crohn's disease, chronic immune thrombovytopaenia CC disease, Guillain-Barre's syndrome, Hashimoto's disease, idiopathic CC mayocadema meastheria cravis necticals nembrices willaris or vertents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteopathic; immunosuppressive; antithyroid; antiinflammatory; antidiabetic; thyromimetic; haemostatic; antipsoriatic; dermatological; antianaemic; immunosuppressive; demyelinating disease; osteoarthritis; inflammatory condition; multiple sclerosis; rheumatoid arthritis; Crohn's disease; chronic immune thrombocytopaenia purpura; colitis; diabetes mellitus; Graves disease; Guillain-Barre's syndrome; psoriasis; Hashimoto's disease; idiopathic myxoedema; myxathenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 glatiramer acetate; autoimmune disease; antiarthritic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY82573 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copolymer 1 related polypeptides used as molecular weight markers for glatiramer acetate and for treatment and prevention of immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pemphigus vulgaris; systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copolymer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000
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myxoedema, myasthenia gravis, psoriasis, pemphigus vulgaris, lupus erythematosus. Mediated-mediated diseases which can be include host-versus-graft disease, graft versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Page 14; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gad A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (YEDA ) YEDA
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PHARM USA INC.
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                                                                              The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences AAA36633-A36652 and peptide sequences AV89456-Y99500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glatiramer acetate molecules, molecular weight markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           delayed-type hypersensitivity. The polypeptides of the invention have defined molecular weights and physical properties which are analogous to glatiramer acetate molecules, which makes them ideal for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transporter system; nucleic acid delivery; gene therapy; cancer; carcinogenesis; cardiovascular disease; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     System for transporting nucleic acid into cells, useful e.g. in therapy and for generating transgenic animals, comprises binding linked to nucleic acid, surface ligand and lytic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-2000
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ligand allows specific targeting of selected cells and tissues. agent provides for release of the nucleic acid into the cellular interior, from endosomes, without requiring endosomal or lysosom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US6033884-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Column 125-128; 108pp; English
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Pred. No. 1.6e-08;
3; Mismatches :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Woo SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
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delivering nucleic acid into a cell. The NTS contains but is not limited to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (b) a molety that recognizes and binds to a cell surface receptor or antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding moiety; (d) a molety that is capable of moving or initiating movement through a nuclear membrane; and/ or (e) a lysis molety that enables the transport of the entire complex from the cell surface directly into the cytoplasm of the cell. The NTS delivers nucleic acid into the cellular interior as well as the nucleus of specific cells. The NTS can be used to treat disorders by targeting specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an
                                                                                                                                                                                                                                                                                                                         14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
                                                                                                                                                                                                          Nucleic acid transport system, useful for creating transgenic for assessing human disease such as cancer in an animal model
                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid transport system; NTS; cell surface receptor; cytosi nuclear membrane; lysis moiety; transgenic animal; human disease;
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                                                                                                                                                         The invention relates to a nucleic acid transport system (NTS)
                                                                                                                                                                                 Disclosure; Columns 123-124; 107pp; English.
                                                                                                                                                                                                                                                                         Woo SLC,
                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-1995;
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92US-0855389.
93WO-US02725.
93US-0167641.
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Pred. No. 3.5
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                                                                                                                                                                                                                                                                         Sparrow J,
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        The sequence represents poly-Lys-Ala, used to bind nucleic acid in a nucleic acid transporter system. The nucleic acid transporter system uses nucleic acid binding complexes containing surface ligands which are capable of binding to a cell surface receptor and entering the cell through cytosis. The compounds of the invention are either ligands, binding molecules (surface ligands), lysis agents, spacer molecules or their intermediates. The ligands, binding molecules, lysis agents and spacer molecules are used in nucleic acid transporter systems to deliver nucleic acid into specific cells e.g. in gene therapy to deliver nucleic acid into hepatocytes, muscle cells or bone forming cells.
                                                                                                                                                                                                                                                                                                            14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 animal model. The NTS can be used in vitro with tissue culture cells which allows the role of various nucleic acids to be studied by targe specific expression into specifically targeted tissue culture cells. lysis agent within the NTS avoids the problem of endosomal/lysosomal
                                                                                                                                                                                     Nucleic acid transport system, useful for creating transgenic for assessing human disease such as cancer in an animal model
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                                                                                                                                                            Disclosure; Column 131; 111pp; English
                                                                                                                                                                                                                                                                                                                                                               05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used in nucleic acid transporter system
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92US-0855389.
93WO-US02725.
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Pred. No. 3.5e-08;
B; Mismatches 3:
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20-MAR-1992;
19-MAR-1993;
                                                                               This invention describes a novel system (I) for delivering a nucleic acid to a cell, comprising a binding complex comprising a ligand binding molecule noncovalently bound to a nucleic acid and covalently linked to a surface ligand, and a second binding complex comprising a second binding molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic acid. The mucleic acid transporter system can also be used in a method for the in vivo targeting of the insertion of DNA into a cell. It can also be used in processes for producing transformed cell lines. The system can be used to deliver a variety or proteins and polypeptides, such as hormones, growth factors, enzymes, clotting factors, apolipoproteins, receptors, drugs, oncogenes, tumor antigens, tumor suppressors, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor; clotting factor; apolipoprotein; tumor antigen; tumor suppressor; viral antigen;
  Sequence
                                                           endosomal/lysosomal degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 125-126; 105pp;
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Pred. No. 3.5e-08
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receptor; drug; oncogene
parasitic antigen;
                                                           art systems
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Query Match

Score 179.5;

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22;

Length 100;

S 밁 S

60 99 Matches Query Match Best Local

Similarity

34.5%;

Conservative

17;

Score 179; DB 24; Pred. No. 1.4e-07; 7; Mismatches 29;

Length 347;

Indels

10;

Gaps

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KKAEKAYAKKAKAAKEK-----KAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKE 59

OKLEOQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKR 158

АУКАЕАККУАКААКАЕККЕУАААЕАККАЕЛАКАУКАЕААКЛЛАКЕЛАУЕА 109

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RESULT 12
ABJ18771
ID ABJ18771
ABJ18771
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XX ABJ18
XX Biofi
KW Cysti
KW Cathe
OX Paeud
XX Paeud
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                                                    The invention comprises a method for identifying a compound capable of modulating biofilm formation by bacteria. The method of the invention is useful for identifying a compound capable of modulating biofilm formation by bacteria or modulating bacterial antibiotic resistance. The method of the invention is also useful for diagnosing and treating a subject (especially an immunocompromised human) that is afflicted with a biofilm-associated disease or disorder, such as: cystic fibrosis; AIDS; middle ear infections; acne; periodontal disease; catheter-associated infections; and medical device-associated infections. The present amino acid sequence represents a protein that is used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biofilm formation modulation; biofilm-associated disease; cystic fibrosis; AIDS; middle ear infection; acne; periodontal disease; catheter-associated infection; medical device-associated infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying compound capable of modulating biofilm formation bacteria/bacterial antibiotic resistance, useful for treatmer biofilm associated disease -
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABJ18771 standard; Protein; 347
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 119-120; 154pp; English.
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(HARD )
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24-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aeruginosa biofilm formation-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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2001US-344142P.
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B; Mismatches
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smatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Greenberg
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159

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                                                                                                                                                                                                                                                                                                      The invention provides heat-killed Mycobacterium vaccae, or recombinant CC M. vaccae proteins. The M. vaccae protein may be employed to activate T cells and natural killer cells, to stimulate the production of CC cytckines, to enhance the expression of co-stimulatory molecules on CC and function. The proteins can be expressed by standard recombinant CC methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the CC treatment, prevention, and detection of disorders including infectious Cdseases, immune disorders and cancer. In particular, the compounds and CC such as mycobacterial infections, asthma, allergies, tuberculosis, CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as gsoriasis, atopic dermatitis, eczema, allergic contact dermatitis, and skin cancers such as basal carcinoma, squamous cell
                                                                                                                   Query Match
Best Local S
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis; dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                       carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 239; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enhancing immune response to an antiger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-430163/36.
N-PSDB; AAZ11393.
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17-SEP-1998;
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23-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dendritic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1997;
                                                                                                                                             Local Similarity
į112
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                                                               μ.
        ARKAAKKAPAKKAAAKKAAPAKKAPAKKA-ATKAAPAKKATAAKKAAPAKKATAAKKAAP 170
                                                 AKKYAKK--AEKAYAKKAKAAKB---KKAYAKKEAKAYKAABAKKKAKAEAKKYAKEAAK 55
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                                                                                                                                                                                                                              223
                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                       melanoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccae protein; antigen; T cell activation; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0997080.
97US-0997362.
98US-0095855.
98US-0156181.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0205426.
97US-0996624.
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                                                                                                                                          34.3%;
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                                                                                                                   6;
                                                                                                                Score 178; DB 20;
Pred. No. 1.1e-07;
6; Mismatches 34
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                                                                                                                                                                    Length 223;
                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder; cancer;
                                                                                                                      10;
                                                                                                                   Gaps
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Conservative

18;

36;

Indels

11;

Gaps

445

AAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEA АККУАККАЕКАУАККАКААКЕККАУАККЕАКАУКААЕАКККАКАЕАККУА----КВААКА 56

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RESULT 14
AAR84568
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                                                                                                   AAR84565-R84569 are polypeptides of the TCR27 protein of T.cruzi
The proteins are all fusion products with glutathione-S-transferase
(GST) and some contain a linker sequence. The TCR27 protein comprises
a 95 amino acid (aa) N-terminal region; 69 repeats of a highly
c conserved 14 as sequence and a 68 as C-terminal region. This sequence
encodes the GST sequence, the Ag44 polypeptide contg. 16 of the 69
repeat units and also contains the amino and carboxy terminal
peptides of TCR27. The TCR27 polypeptides of the invention are useful
for the diagnosis of Chagas disease (American Trypanosomiasis), they
are capable of detecting anti-T.cruzi antibodies; or for blood
screening. The TCR27 protein has epitopes to which most T.cruzi
infected individuals have antibodies. The TCR27 polypeptides will not
react with serum from patients with leishmaniasis, schistosomiasis,
or autoimune disease and are hence less likely to cause false
    Best Loc
Matches
                                Query Match
                                                                                                                                                                                                                                                                                                                                                             New polypeptide(s) from the TCR27 protein of Trypanosoma cruzi - immunoassay reagent for specific diagnosis of Chagas disease, also related nucleic acid and transformed cells
                                                            Sequence
                                                                                                                                                                                                                                                                                                                                Disclosure; Page 40-41; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAT05332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCR27; Chagas disease; repeat unit; diagnosis; blood screening; recombinant; fusion protein; glutathione-S-transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR84568;
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-344618/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kirchhoff LV, Otsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KIRC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09525797-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR84568 standard; Protein;
Local Similarity
les 52; Conserv
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OTSU K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKKBAYKABAKKYAKAAKABKKEYA--AABAKKABAAKAYKABAAKAAAK 103
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                                                              .643 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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/note= "16 of 69 repe
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                  31.3%;
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Pred. No. 6.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a method for the diagnosis, prevention and CC treatment of ulcerative colitis (UC) using histone H1-like antigen, a composition antigen or a Bacteroides antigen as a target antigen. The novel method of diagnosing UC in a subject suspected of having inflammatory bowel disease (IBD) comprises: (1) obtaining a sample from the subject; (2) contacting the sample with a histone H1-like antigen, or perinuclear anti-neutrophil cytoplasmic antibody (pANCA)-reactive fragment, to form a complex of the histone H1-like antigen, or the pANCA-reactive fragment, and antibody to the histone H1-like antigen, or the pANCA-reactive fragment, confidence or absence of the complex; where the presence of the complex confidence of the complex of indicates that the subject has UC. The pANCA-reactive histone H1-like antigen, porin antigen and Bacteroides antigen are useful in the confidence of identifying agents useful for treating UC. The methods can also be used for identifying agents useful for treating UC. The present sequence confidence in the complex useful for treating UC. The present sequence confidence is a human histone H1 isoform H1.5 pANCA-reactive fragment.
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of histone H1, porin or Bacteroides antigens as targets for the diagnosis, prevention and treatment of ulcerative colitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-551215/46
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                                                                                                                                                                                                                                                                                        51; Conservative
                                                                                                                                                                                                                1 АККҮАККАЕКАҮАККАКААКЕККАҮАККЕАКАҮКАА-----ЕАКККАКАЕАККҮАКЕААК 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEAA 561
                                                                    АККЕЛУКАЕЛККУАКЛАКЛЕККЕУЛЛАЕЛККАЕЛЛКАУКЛЕЛЛКЛАЛКЕ 104
                                                                                                                                                AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 108
AKAAAKPKKATKSPAKPKAVKPKAAKPKAAKPKAAKPKAAKAKKAAAKK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                     158 AA;
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Pred. No. 2.2e-06;
7; Mismatches 44;
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Search completed: January 21, 2004, 08:59:10

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Perfect score:
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Match Length
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/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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US-10-127-032-120
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US-10-051-643-201
US-10-156-761-9889
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Sequence 31, Appl
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ALIGNMENTS

US-09-816-989A-7

Sequence 7, Application US/09816989A Patent No. US20020115103A1

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TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REPERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 7
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Best Local Similarity
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TYPE: PRT
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PRAMIES.
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Pred. No. 1.9e-34;
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                                                                             Query Match 55.7%;
Best Local Similarity 67.0%;
Matches 73; Conservative
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SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide -09-816-989A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09816989A
Patent No. US20020115103A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic -09-816-989A-6
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APPLICANT: Lis, Doris
TITLE OF INVENTION: COPPLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
TITLE OF INVENTION: AND FOR THERAPEUTIC USE
FILE REFERENCE: 2609/60807-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/816,989A
CURRENT FILING DATE: 2001-03-23
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/101,693
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: PCT/US99/22402
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARY TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gad, Alexander APPLICANT: Lis, Doris
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                           ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US99/22402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6, Application US/09816989A
). US20020115103A1
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                          AKKYAKKAEKAYAKKAKAAKEKKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKEA 60
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  AKKYAKK-EKAYAKKA----EKAAKKAEAKAYKAAEAKKKA-
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1; Mismatches
                                                                           Score 289; DB 10;
Pred. No. 2.1e-16;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.2e-18;
                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                        Length 77;
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US-09-816-989A-3
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US-09-816-989A-4
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LENGTH: 66
TYPE: PRT
                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 56
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US Patent No. US20020115103A1
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APPLICANT: Gad, Alexander
APPLICANT: Lis, Doris
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Patent No. US20020115103A1
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                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR PILING DATE: 1998-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES TITLE OF INVENTION: AND FOR THERAPEUTIC USE FILE REFERENCE: 2609/60807-A-PCT-US CURRENT APPLICATION NUMBER: US/09/816,989A CURRENT FILING DATE: 2001-03-23 PRIOR APPLICATION NUMBER: 60/101,693 PRIOR FILING DATE: 1998-09-25 PRIOR APPLICATION NUMBER: FCT/US99/22402 PRIOR APPLICATION NUMBER: PCT/US99/22402 PRIOR FILING DATE: 1999-09-24 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US99/22402 PRIOR FILING DATE: 1999-09-24
                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 7
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                                                                              FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAAYEA 109
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34.8%;
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Pred. No. 1.1e-11;
  Score 180.5; DB 10;
Pred. No. 5.8e-08;
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; TYPE: PRT ; ORGANISM: Mycobacterium vaccae US-10-205-979-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
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; ORGANISM: Pseudomonas aeruginosa
US-10-127-032-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-127-032-120
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                                                          SEQ ID NO 52
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                       Sequence 52, Application US/10205979 Publication No. US20030147861A1
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Best Local Similarity
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                                                                                            TITLE OF INVENTION: Compounds and Methods for the Modulation TITLE OF INVENTION: of Immune Responses FILE REFERENCE: 11000.1063U

CURRENT APPLICATION NUMBER: US/10/205,979

CURRENT FILING DATE: 2002-07-25

PRIOR APPLICATION NUMBER: 60/308,446

PRIOR FILING DATE: 2001-07-26

PRIOR FILING DATE: 2001-07-26

NUMBER OF SEQ ID NOS: 52

SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: US 60/344,142
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Greenberg, Everett Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE MODULATION
TITLE OF INVENTION: BIOFILM FORMATION
FILE REFERENCE: UIZ-070CP
                                                                                                                                                                                                                                                                                     APPLICANT: Watson, APPLICANT: Tan, PAPPLICANT: Aberne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/127,032
CURRENT FILING DATE: 2002-04-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Whiteley, Marvin APPLICANT: Bangera, M. Gita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uence 120, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 A-EDEAKK--KAAEDAKKK-AAEDAKKKAAEEAKKKAAAEAAKKKAAVEA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 АУКАЕАККҮАКААКАЕККЕУАААЕАККАЕААКАУКАЕААКААКЕААУЕА 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 OKLEQQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 ККАЕКАУАККАКААКЕК-----КАУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕ 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50; Conservative
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                                                                                                                                                                                                                                                                                     Tan, Paul L. J.
Abernethy, Nevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lory, Stephen
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                                                                                                                                                                                                                                                                                                                                James D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 179; DB 15; Length 347; Pred. No. 5e-07;
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US-10-051-643-201
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US-10-156-761-9889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 201
LENGTH: 223
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Publication No. US20020197265A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 54.9 Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                     Sequence 9889, Application US/10156761 Publication No. US20030119018A1
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                                                                                                                                                                                                                                               APPLICANT:
               CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 11000.1008c2
CURRENT APPLICATION NUMBER: US/10/051,643
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US09/156,181
PRIOR FILING DATE: 1998-09-17
                                                                                                                                                                                                                                                                                        APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 08/996,624 PRIOR FILING DATE: 1997-12-23 NUMBER OF SEQ ID NOS: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Methods and Compounds for the Treatment
TITLE OF INVENTION: of Immunologically-Mediated Diseases of the Respiratory
TITLE OF INVENTION: System using Mycobacterium Vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Watson, James D. APPLICANT: Tan, Paul L. J.
                                                                                                                                                           APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                            FILE REFERENCE: 249-262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARKAAKKAPAKKAAAKKAAPAKKAPAKKA-ATKAAPAKKATAAKKAAPAKKATAAKKAAP 170
                                                                                                                                                                                                                                                 HORIKAWA, JUN
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Pred. No. 3.8e-07;
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Pred. No. 3.8e-07
5; Mismatches 3
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RESULT 11
US-10-229-567-40
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; OTHER INFORMATION: gi|9656364
US-09-820-843A-27
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Publication No. US20030039963A1
GENERAL INFORMATION:
APPLICANT: Council of Scientific and Industrial Research
TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION
TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
FILE REFERENCE: 063915
FILE REFERENCE: 063915
                                                                                                                                                                        Sequence 40, Application US/10229567 Publication No. US20030092080A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/820,843A
CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 356
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Best Local Similarity
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Best Local Similarity
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 376
TYPE: PRT
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OTHER INFORMATION: tola protein
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                                                                       TITLE OF INVENTION: Diagnosis, Prevention and Treatment of Ulcerative Colitis, and Clinical Subtypes Microbial UC pANCA antigens
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbel
                                                       NUMBER OF SEQUENCES:
                                                                                                                                  APPLICANT: Braun, Jonathan
Cohavy, Offer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305
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                                                                                                                                                                                                                                                                                                                                                                                                                        57 KKEAYKAEAKKYAK------AAKAEK----KEYAAAEAKKAEAAKAYKAEAAKA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ККАЕКАУАККАКАКАКЕ---ККАУАККЕАКАУКААЕАК---ККАКАЕАККУАКЕААКАККЕ
                                                                                                                                                                                                                                                                                                                                                AAKEAAYEA 109
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ADDRESSEE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite 700
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42.6%; Pred. No. 1.1e-05;
ative 13; Mismatches 37;
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44.9%; Pred. No. 9.9e-06;
ative 15; Mismatches 38;
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LENGTH: 158 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-229-567-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 30.9%;
Local Similarity 46.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/417,264
PILING DATE: «Unknown»
APPLICATION NUMBER: US 09/041,889
PILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Diagnosis, Prevention and Treatment Ulcerative Colitis, and Clinical Sul Microbial UC panch antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 АККУАККАЕКАУАККАКААКЕККАУАККЕАКАУКАА-----ЕАКККАКАЕАККУАКЕААК 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKAAAKPKKATKSPAKPKAVKPKAAKPKAAKPKAAKPKAAKAKKAAAKK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         АККЕАУКАЕАККУАКААКАЕККЕУАЛАЕАККАЕЛАКАУКАЕЛАКАЛАКЕ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
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STATE: California
                                                                                                                                                                                                                       CITY: San Diego
STATE: California
                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10229567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 6.4e-06;
                                                                     Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version
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LENGTH: 226 amino acids

TYPE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-229-567-32
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US-10-262-209-1
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문
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Best Local Similarity 46.8%;
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10262209
Publication No. US20030125239A1
                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
                                                                                                                                                                                                                                         -10-262-209-1
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: UK 0218324.2
PRIOR FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: PCT/GB01/01699
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: UK 0102667.3
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: UK 0009080.3
                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Crisanti, Andrea APPLICANT: Esseghir, Selma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: GJE-6703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Esseghir, Selma
                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                 LENGTH: 234
                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE: «Unknown»
APPLICATION NUMBER: US 09/041,889
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
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167
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                                   60 АУКАЕАККҮАКААКАЕККЕУАААЕАК-----КАЕААКАУКАЕААКААКААКЕААУЕ 108
                                                                                                                                                            53;
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AKKAKSPKKAKAAKPKKAPKSPAKAKAVKPKAAKPKTAKPKAAKPKKAAAKKKKLE 222
                                                                               KKAASGEAKPKAKKAGAAKAKPAGAAKKPKKATGAATPKKSAKKTPKKAKKPAAAA--G
                                                                                                                KKYAKKAEKAYAKKAKAAKEKK--AYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAKAKKE 59
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TELEFAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
                                                                                                                                                            Conservative
                                                                                                                                                                            30.7%;
45.7%;
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Pred. No. 9.3e-06;
                                                                                                                                                                          Score 159.5; DB 1
Pred. No. 1.2e-05;
                                                                                                                                                            Mismatches
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US-10-229-567-4
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                                                                                                                                                                 Query Match
Best Local Similarity
Matches 53; Conserv
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE: <UNKnown>
APPLICATION NUMBER: US 09/041,889
FILING DATE: <UNKnown>
ATTORNEY/AGENT IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Diagnosis, Prevention and Treatment of Ulcerative Colitis, and Clinical Subtypes Thereof, Using Microbial UC pANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Braun, Jonathan
Cohavy, Offer
                                                                                    108 KKAASGEAKPKAKKAGAAKAKKPAGAAKKPKKATGAATPKKSAKKTPKKAKKPAAAA--G 165
166 AKKAKSPKKAKAAKPKKAPKSPAKAKAVKPKAAKPKTAKPKAAKPKKAA 214
                                       60 АУҚАБАКҚУАҚААҚАБҚ--КБУАААБАККАБААҚАУҚАБААҚААҚБАА 106
                                                                                                                              N
                                                                                                                            ККУАККАЕКАУАККАКААКЕКК--АУАККЕАКАУКААЕАКККАКАЕАККУАКЕААКАККЕ 59
                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
H1-S-4"
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 218 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Campbell & Flores LLP STREET: 4370 La Jolla Village Drive, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619)
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                                                                                                                                                                        Conservative
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1..218
                                                                                                                                                                                        30.4%;
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                                                                                                                                                                    Score 158; DB 15;
Pred. No. 1.4e-05;
7; Mismatches 43;
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                                                                                                                                                                                                           Length 218;
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RESULT 15 US-10-262-209-2

Sequence 2, Application US/10262209
Publication No. US20030125239A1
GENERAL INFORMATION:
APPLICANT: Crisanti, Andrea

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Page 6
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APPLICANT: EBSeghir, Selma
TITLE OF INVENTION: Compositions for Drug Delivery
FILE REFERENCE: GLE-6703
CURRENT FILING DATE: 2002-09-30
CURRENT PILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: UK 0218324.2
PRIOR APPLICATION NUMBER: PCT/GB01/01699
PRIOR APPLICATION NUMBER: UK 0218324.2
PRIOR FILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PRICATION NUMBER: UK 0009080.3
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
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PRIOR PILING DATE: 2001-04-12
PRIOR PILING
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Maximum Match 100%
Listing first 45 summaries
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

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Sequence 1, Appl	Sequence 1, Appl:	Sequence 1, Appl	Sequence 2, Appl	Sequence 62, App	Sequence 62, App	Sequence 62, App	Sequence 62, App	Sequence 27, App	Sequence 27, App	Sequence 3, Appl	Sequence 3, Appl:	Sequence 22853,	· Sequence 5, Appli	Sequence 32957,	Sequence 3, Appli	Sequence 3, Appl	Sequence 3, Appl

ALIGNMENTS

RESULT 1 US-09-405-743A-7

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CURRENT FILING DATE: 199-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 7
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
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Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
                                                                                                       GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn VG
SEQ ID NO 6
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Best Local Similarity
                LENGTH: 80
TYPE: PRT
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ORGANISM: Artificial Sequence
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Pred. No. 4.7e-37;
Mismatches 0;
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OTHER INFORMATION: PEPTIDE
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Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd.
APPLICANT: Yeda Research and Development Co., Ltd.
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5
LENGTH: 77
                                                                                                                   FILE REFERENCE: 60807-A
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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                                                LENGTH: 66
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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TYPE: PRT
ORGANISM: Artificial Sequence
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Pred. No. 6.5e-20;
1; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 289; DB 4;
Pred. No. 5.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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RESULT 6
US-08-460-890A-64
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; OTHER INFORMATION:
US-09-405-743A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09405743A
Patent No. 6514938
GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co., Ltd
TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR
FILE REFERENCE: 60807-A
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: WOO, Sa
APPLICANT: Smith,
APPLICANT: Cristia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity 45.9%;
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                                                                                                                                                                                                                                                                                                                                            Patent No. 5994109
                                                                                                                                                                                                                                                                                                                                                         Sequence 64, Application US/08460890A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 60807-A.
CURRENT APPLICATION NUMBER: US/09/405,743A
CURRENT FILING DATE: 1999-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 56
                                           COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth S
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                  APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: MUCLEIC ACID TRANSPORTER SYSTEMS AND
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 44.0%;
Local Similarity 56.9%;
                 COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.O
   SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKAEAKKYAKAAKAEKKEYAAAEAKKAEAAKAYKAEAAKAAKEAAYEA
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                                                                                                                                                                                                                                                                                                 Smith,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
SYSTEM: IBM P.C. DOS 5.0 FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                              Savio L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description of Artificial Sequence: PEPTIDE
                                                                                                                                                                                                                                                                                               Louis C
                                                                                                                                                                        Street
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Pred. No. 5.2e-13;
0; Mismatches 4;
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Pred. No. 4.5e-09;
                                                                1.44 Mb
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,890A FILING DATE: June 5, 1995

CLASSIFICATION:

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                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6033884
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 64,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02
FILING DATE: March 19, 1993
ATTORNEY/ACENT INFORMATION:
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: Lyon & Ly
                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEIC ACID TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: "Lys Ala" in positions 3 to
OTHER INFORMATION: present or absent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              APPLICANT: Cristiano, Richard J. APPLICANT: Gottchalk, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                            OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                            STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard REGISTRATION NUMBER: 37
                                                                                                                                                                                               CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ropology:
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                                                                                                                                                                               California
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Smith, Louis C.
                                                                                                                                                                U.S.A.
                                            IBM Compatible
SYSTEM: IBM P.C. DOS 5.1
FastSEQ for Windows 2.0
                                                                                                                                                                                                                                             Lyon & Lyon
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December 14, 1993
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             US/08/167,641C
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Pred. No. 9.7e-09;
                                                                                                                                                                                                                                                                                                                ACID TRANSPORTER SYSTEMS AND
                                                             DOS 5.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-167-641C-64
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Best Local Similarity
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
APPLICATION NUMBER: 07/1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/167,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: PastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
THE APPLICAT
                                                                                                                                                                                                                                                                                                                                                               ZIE: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NUCLEIC ACID TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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STRANDEDNESS: sir
TOPOLOGY: linear
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REGISTRATION NUMBER: 32,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: "Lys Ala" in positions 3 OTHER INFORMATION: present or absent.
                                                                                                                                                  FILING DATE:
                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 ККАЕКАУАК-КАКААКЕККАУАККЕАКАУКААБАКККАКАБАККУАКБААКАККЕАУКАБ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08460971A
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                                                                                                                                           June 5, 1995
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December 14,
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55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEIC ACID TRANSPORTER SYSTEMS
                                                                                                                                                                                                                                                                                                  IBM P.C. DOS 5.0
                                                                                                                                                                                 US/08/460,971A
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Pred. No. 9.7e-09;
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March 20, 1992 UMBER: PCT/US93/02725

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Best Local Similarity
                                                                                                       SOFTWARE: FASTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTESS for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,040
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION: 536
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INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 65 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WOO, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
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LENGTH: 100 amino acid
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APPLICATION NUMBER: PCT/US9:
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                     FILING DATE: June 5,
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
FILING DATE: December 14, 1993
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20,1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19,1993
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                       COMPUTER: IBM Con
OPERATING SYSTEM:
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STRANDEDNESS: sir
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6177554
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: California
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                                                                                       08/167,641
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Pred. No. 9.7e-09;
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US-09-095-855-201 RESULT 11

Sequence 201, Application US/09095855 Patent No. 6160093 GENERAL INFORMATION:

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US-09-252-991A-29581
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                                                                                                                                                                                                                                                                                                                         PATENT APPLICATION NUMBER: US/69/252,991A

CURRENT APPLICATION NUMBER: US/69/252,991A

CURRENT APPLICATION NUMBER: US/69/252,991A

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SEQ ID NO 29581
LENGTH: 407
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Best Local Similarity
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                 TYPE: PRT
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LENGTH: 100 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
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TOPOLOGY: linear
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/078
                                                                                                                                              Match 34.5%; Score 179; DB 4; Local Similarity 49.1%; Pred. No. 4.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: OTHER INFORMATION:
219 A-EDEAKK--KAAEDAKKK-AAEDAKKKAAEEAKKKAAAEAAKKKAAVBA 264
                                                                159 QKLEQQQVAAAKAAEQKKADEARKAEAQKAAEAKKADEAKKAAEAKAAEQKKQADIAKKR
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                                                                                              6 ККАЕКАУАККАКАКАКЕК-----КАУАККЕАКАУКААЕАКККАКАЕААККУАКЕААКАККЕ 59
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                              АУКАБАККУАКААКАЕККЕУАААЕАККАЕААКАУКАЕААКАААКЕААУЕА 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         АККҮАКА-АКАЕККЕҮАААЕАККАЕААКАҮКАЕААКААК 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 9.7e-09;
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                                                                                                                                                                Length 407;
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RESULT 12
US-09-205-426-201
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// MOLECULE TYPE: protein
US-09-095-855-201
                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                Sequence 201, Application US/09205426 Patent No. 6406704
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                             APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L. J.
TITLE OF INVENTION: Compounds and Methods for Treatment and
TITLE OF INVENTION: Diagnosis of Mycobacterial infections
FILE REFERENCE: 11000.1002c4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION NUMBER: US/09/205,426
CURRENT FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/87
FILING DATE: 12-JUN-1997
APPLICATION NUMBER: 08/997
APPLICATION SATE: 23-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sleath, Janet REGISTRATION NUMBER: 37,007 REFERENCE/DOCKET NUMBER: 111 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Compounds and Methods for TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections NUMBER OF SEQUENCES: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tan, Paul
APPLICANT: Visser, Eli
APPLICANT: Skinner, Ma
APPLICANT: Prestidge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                112 АККЛАККАРАККАЛАККАЛРАККАРАККА-АТКАЛРАККАТЛАККАЛРАККАТАЛККАЛР 170
                                                                                                                                                                                                                                                                                                   56 АККЕЛҮКАЕЛККҮАКЛАКЛЕККЕҮЛ--ЛЛЕЛККАЕЛЛКАЕЛЛКАЕЛЛКАЛАК 103
                                                                                                                                                                                                                                                                                                                                                                                                                    60;
                                                                                                                                                                                                                                                                                                                                                                           1 AKKYAKK--AEKAYAKKAKAAKE----KKAYAKKEAKAYKAAEAKKKAKAEAKKYAKEAAK 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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Skinner, Margot
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Law Offices of Ann W. Speckman
01 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201:
                                                                                                                                                                                                                                                                                                                                                                                                                Score 178; DB 3;
Pred. No. 2.9e-08;
6; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11000.1002c3
                                                                                                                                                                                                                                                                                                                                                                                                                  34; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 223;
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; MOLECULE TYPE: protein US-08-216-894-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-216-894-8
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LENGTH: 223
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Patent No. 587673
Matches
                Query Match
Best Local Similarity
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Best Local
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EARLIER APPLICATION NUMBER: 08/705,347
EARLIER FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 208
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,894
PILING DATE: 24-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-06-11
EARLIER APPLICATION NUMBER: 08/997,362
EARLIER FILING DATE: 1997-12-23
EARLIER APPLICATION NUMBER: 08/873,970
                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                   NAME: BENT Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kirchhoff, Louis V.
APPLICANT: Otsu, Keiko
TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 300.
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TELEX: 904136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 АККЛАККАРАККАЛАККАЛРАККАРАККА-АТКАЛРАККАТАЛККАЛРАККАТАЛККАЛР 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 АККЕЛУКЛЕЛККУЛКЛАКЛЕККЕУЛ--ЛЛЕЛККАЕЛЛКАУКЛЕЛЛКАЛАК 103
52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08216894
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3000 K Street, N.W., Suite 500
Mashington, D.C.
                                                                                                                                                                                                                                   (202) 672-5399
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.3%;
                  31.3%; Score 162.5; DB 2 44.4%; Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                         US/08/216,894
                                                                                                                                                                                                                                                                                                                                                                                                                               Release #1.0, Version #1.25
                                                                                                                                                                                            8.
  18;
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Pred. No. 2.9e-08; 
6; Mismatches 34; Indels
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  Mismatches
                                    DB 2;
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  36;
Indels 11;
                                    Length 643;
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US-09-115-746-8
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                                                                                                                                             RESULT 15
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Best Local S
Matches 52
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Patent No.
                                                                     Sequence 40, Applicat Patent No. 6033864 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Braun, Jonathan APPLICANT: Cohavy, Offer TITLE OF INVENTION: Diagnos TITLE OF INVENTION: Ulcerat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Otbu, Keiko
TITLE OF INVENTION: POLYBEPTIDES FOR DIAGNOSING INFECTION
TITLE OF INVENTION: WITH TRYPANOSOMA CRUZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kirchhoff, Louis V. APPLICANT: Otsu, Keiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                    445 AAEATKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEATKVAEAEKOKAAEA 504
                                                                                                                                                                                              505 TKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEATKVAEAEKQKAAEAA 561
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5. 6228601
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                                                                                                                                                                                                                                                                                              1 AKKYAKKAEKAYAKKAKAKAKKKAYAKKEAKAYKAAEAKKKAKAEAKKYA----KEAAKA 56
                                                                                        0, Application US/09041889
6033864
                                                                                                                                                                                                                                                                                                                                      Similarity 44.4
52; Conservative
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3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : (202)672-5300
(202)672-5399
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44.4%; Pred
44.1%; 18;
 Diagnosis, Prevention and Treatment of Ulcerative Colitis, and Clinical Subtypes Thereof, Using
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                                                                                                                                                                                                                                                                                                                                      Score 162.5; DB 3;
Pred. No. 1.6e-06;
8; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suite 500
                                                                                                                                                                                                                                                                                                                                                                       Length 643;
                                                                                                                                                                                                                                                                                                                                        Indels
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US-09-041-889-40
                                                                                                                                                                       Query Match
                                                                                                                                        Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, 1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Microbial UC pANCA antigens NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                           TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Diego
STATE: California
                                                                                                                30.9%;
Local Similarity 46.8%;
es 51; Conservative
                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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109
                                                                     51
                                  56
 AKAAAKPKKATKSPAKPKAVKPKAAKPKAAKPKAAKPKAAKKAKKAAAKK 157
                                  АККЕАУКАЕАККУАКААКАЕККЕУАЛАЕАККАЕЛАКАУКАЕЛАКАААКЕ 104
                                                                     AKPKAKKAGAAKAKKPAGATPKK--AKKAAGAKKAVKKTPKKAKKPAAAGVKKVAKSPKK 108
                                                                                                    АККУАККАЕКАУАККАКААКЕККАУАККЕАКАУКАА----ЕАКККАКАЕАККУАКЕААК 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                    (619)
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                                                                                                                                      Score 160.5; DB :
Pred. No. 5.9e-07;
7; Mismatches 4
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                                                                                                                                                                           DB 3;
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                                                                                                                                          44;
                                                                                                                                          Indels
                                                                                                                                                                           Length
                                                                                                                                                                             158;
                                                                                                                                          7;
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Search completed: January 21, 2004, 09:02:21 Job time: 21.526 secs

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